

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

## STAFF USE ONLY

Searcher: \_\_\_\_\_

Searcher Phone #: \_\_\_\_\_

Searcher Location: \_\_\_\_\_

Date Searcher Picked Up: 8/20/01

Date Completed: 8/21/01

Searcher Prep & Review Time: \_\_\_\_\_

Clerical Prep Time: \_\_\_\_\_

Online Time: \_\_\_\_\_

## Type of Search

NA Sequence (#) 1

AA Sequence (#) 1

Structure (#) \_\_\_\_\_

Bibliographic \_\_\_\_\_

Litigation \_\_\_\_\_

Fulltext \_\_\_\_\_

Patent Family \_\_\_\_\_

Other \_\_\_\_\_

## Vendors and cost where applicable

STN \_\_\_\_\_

Dialog \_\_\_\_\_

Questel/Orbit \_\_\_\_\_

Dr. Link \_\_\_\_\_

Lexis/Nexis \_\_\_\_\_

Sequence Systems 03

WWW/Internet \_\_\_\_\_

Other (specify) \_\_\_\_\_

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2001, 21:25:24 ; Search time 1076.8 Seconds  
(without alignments)  
7325.921 Million cell updates/sec

Title: US-09-461-646-l\_COPY\_667\_1176  
Perfect score: 510  
Sequence: 1 gcggctaccgactggaaga.....agatgtacggagacatggca 510

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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  - 2: gb\_ba2:\*
  - 3: gb\_ba3:\*
  - 4: gb\_in1:\*
  - 5: gb\_in2:\*
  - 6: gb\_in3:\*
  - 7: gb\_om:\*
  - 8: gb\_ov:\*
  - 9: gb\_pat1:\*
  - 10: gb\_pat2:\*
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- 91: gb\_pr7:\*
- 92: gb\_pr8:\*
- 93: gb\_pr9:\*
- 94: gb\_ro1:\*
- 95: gb\_ro2:\*
- 96: gb\_in4:\*
- 97: gb\_pr10:\*
- 98: em\_ba3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	510	100.0	1900	97	HSU14750	U14750 Human conne
2	510	100.0	2075	9	AR018957	AR018957 Sequence
3	510	100.0	2075	10	I11636	I11636 Sequence 1
4	510	100.0	2075	10	I32210	I32210 Sequence 1
5	510	100.0	2075	97	HUMCONRO	M92934 Human conne
6	510	100.0	2312	93	HSCITGF	X78947 H.sapiens m
7	451.4	88.5	1598	7	U70060	U70060 Sus scrofa
8	451.4	88.5	2330	7	BTAF000137	AF000137 Bos tauru

us-09-461-646-1\_copy\_667\_1176.rge

Tue Aug 21 08:16:51 2001

AUTHORS Sutter, T.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-SEP-1994) Thomas R. Sutter, Toxicological Sciences,  
 Hygiene 7032, Johns Hopkins University, 615 North Wolfe Street,  
 Baltimore, MD 21205, USA

FEATURES  
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 Location/Qualifiers  
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CDS  
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 1893..1898  
 513 a 420 c 462 g 505 t  
 BASE COUNT  
 ORIGIN

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 378 ctggttcagacacacagagtgagcgtgttccagacacctggtggtatgggcatctccacc 180  
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 618 cgagctaaatctgagtgatgtaccgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc

U83916 Sus scrofa  
 M70642 Mouse Fisp-  
 M80263 Mouse mRNA  
 AB023068 Rattus no  
 AF120275 Rattus no  
 AJ298335 Gallus ga  
 AJ271167 Notophtha  
 U43524 Xenopus lae  
 AL354866 Human DNA  
 AX034368 Sequence  
 AX034367 Sequence  
 AF079531 Rattus no  
 AF309555 Bos tauru  
 M70641 Mouse Fisp-  
 U43523 Xenopus lae  
 X96584 H. sapiens m  
 U37063 Xenopus lae  
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 A28444 nov mRNA se  
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 Y09257 M.musculus  
 X96585 M.musculus  
 U13063 Coturnix ja  
 X97863 M.musculus  
 BC003774 Mus muscu  
 AF171936 Rattus no  
 E13814 cDNA encodi  
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 AF003594 Homo sapi  
 BC001271 Homo sapi  
 U62015 Homo sapien  
 Y12084 H. sapiens m  
 Z98053 Homo sapien  
 Y11307 H. sapiens C  
 AX035239 Sequence  
 AB015877 Rattus no  
 AF218568 Rattus no

ALIGNMENTS

RESULT 1  
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 LOCUS Human connective tissue growth factor mRNA, partial cds.  
 DEFINITION  
 ACCESSION U14750  
 VERSION U14750.1 GI:984955  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1900)  
 Cody, C.W., Walker, N.J., Greenlee, W.F. and Sutter, T.R.  
 Connective tissue growth factor mRNA is expressed in human  
 keratinocytes as an immediate early gene that responds to serum,  
 EGF, or wounding.  
 J. Cell Biol. 114 (6), 1283-1294 (1991)  
 Unpublished  
 2 (bases 1 to 1900)  
 Sutter, T.R., Guzman, K., Dold, K.M. and Greenlee, W.F.  
 Targets for dioxin: genes for plasminogen activator Inhibitor-2 and  
 Interleukin-1 beta  
 Science 254 (5030), 415-418 (1991)  
 3 (bases 1 to 1723)  
 Bradham, D.M., Igarashi, A., Potter, R.L. and Grotendorst, G.R.  
 Connective tissue growth factor: a cysteine-rich mitogen secreted  
 by human vascular endothelial cells is related to the SRC-induced  
 immediate early gene product CEF-10  
 J. Cell Biol. 114 (6), 1283-1294 (1991)  
 J9373462  
 4 (bases 1 to 1900)  
 JOURNAL MEDLINE  
 REFERENCE 4



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QY 361 accctgcccgtgagttcaagtccctgacgagcgaggtcatgaagaagaacatgatgttc 420
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RESULT 2
LOCUS AR018957 2075 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5783187.
ACCESSION AR018957
VERSION AR018957.1 GI:3974071
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2075)
AUTHORS Grotendorst,G.R. and Bradham,D.M. Jr.
TITLE Treatment of cell proliferative disorders using antibodies which
bind connective tissue growth factor
JOURNAL Patent: US 5783187-A 1 21-JUL-1998;
FEATURES Location/Qualifiers
source 1..2075
BASE COUNT 491 a 558 c 546 g 480 t
ORIGIN

Query Match 100.0%; Score 510; DB 9; Length 2075;
Best Local Similarity 100.0%; Pred. No. 6.4e-131;
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 agcccttgcaagctgacctggagagaaacattaaagagggcaaaaagtgcattccgtact 240
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RESULT 3
LOCUS I11636 2075 bp DNA PAT 20-MAR-1996
DEFINITION Sequence 1 from Patent US 5408040.
ACCESSION I11636
VERSION I11636.1 GI:909154
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2075)
AUTHORS Grotendorst,G.R. and Bradham,D.M. Jr.
TITLE Connective tissue growth factor(CTGF).
JOURNAL Patent: US 5408040-A 1 18-APR-1995;
FEATURES Location/Qualifiers
source 1..2075
BASE COUNT 491 a 558 c 546 g 480 t
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Query Match 100.0%; Score 510; DB 10; Length 2075;
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Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS I32210 2075 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5585270.
ACCESSION I32210
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LOCUS	HSCTGF	2312 bp	mrna	PRI
DEFINITION	H.sapiens mRNA for connective tissue growth factor.			10-MAR-1997
ACCESSION	X78947			
VERSION	X78947.1	GI:474933		
KEYWORDS	connective tissue; growth factor.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Oemar, B.S., Werner, A., Garnier, J.M., Do, D.D., Godoy, N., Nauck, M., Marz, W., Rupp, J., Pech, M. and Lüscher, T.F.			
TITLE	Human connective tissue growth factor is expressed in advanced atherosclerotic lesions			
JOURNAL	Circulation 95 (4), 831-839 (1997)			
MEDLINE	9720746			
REFERENCE	2 (bases 1 to 2312)			
AUTHORS	Oemar, B.S.			
TITLE	Direct Submission			
JOURNAL	Submitted (22-APR-1994) B.S. Oemar, University Hospital Basel, Dept of Research, Lab of Vascular Research, Hebelstr. 20, 4031 Basel, SWITZERLAND			
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0;				
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Db	803	CGGTTTACCAATGACAAACGCCTCTCTGAGGCTAGAGAAGCAGAGCCGCTCTG	240	
Qy	181	aggcttgcgaagctgacctggaagaagaacatttaagaaggcgaagtgcatcgctact	240	
Db	863	AGGCTTTCCGAAGCTGACCTGGGAAGAACATTAAAGAGGCAAAAGTGCATCCGTACT	300	
Qy	241	cccaaatctccaaagcctatcaagtcttgagctttctgctgacccagcagcagacatac	300	
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DEFINITION	Sus scrofa connective tissue growth factor (CTGF) mRNA, complete cds.			05-JAN-1999
ACCESSION	U70060			
VERSION	U70060.1	GI:4097832		
KEYWORDS				
SOURCE	pig.			
ORGANISM	Sus scrofa			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
AUTHORS	Harding, P.A. and Brigstock, D.R.			
TITLE	Cloning and sequencing of a porcine connective tissue growth factor (CTGF) cDNA			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 1598)			
AUTHORS	Harding, P.A. and Brigstock, D.R.			
TITLE	Direct Submission			
JOURNAL	Submitted (09-SEP-1996) Surgery, Children's Hospital, 700 Children's Drive, Columbus, OH 43205, USA			
FEATURES	Location/Qualifiers			
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Tue Aug 21 08:16:51 2001

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567 a 624 c 551 t
BASE COUNT 567 a 624 c 551 t
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Best Local Similarity 92.9%; Pred. No. 1.2e-114; Indels 0; Gaps 0;
Matches 473; Conservative 0; Mismatches 36;
1 qcggcttaccgactggaagacacgtttgcccagacaccccaactatgattagagcaactgc 60
Db 743 GCAGCTTACCGGTGGAGACACAGCTTTGGCCAGACACCCACCATGATCCGAGCCACTGC 802
Qy 61 ctggtccagaccacagatggagcgccttcccaagacctgtgggatgggcatctccacc 120
Qy 803 CAGGTCCAGACACAGATGGAGTGCCTATTCCAGACCTGCGGAATGGCATCTCCACC 862
Db 121 cgggttaccatgacacgcctctcctgagctagagaaagacagcgcctgtgcatggtc 180
Qy 863 CGGGTTACCATGACACGCATTTCTGAGGCTGGAGAGCAGAGCCGCTCTGCTGATGTC 922
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Qy 301 cgaagctaatctgtgagatgtgtaccagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1102
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Db 421 atcaagacctgtgctgctccattacactgtcccgagacacacacacacacacacacac 480
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RESULT 9
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LOCUS Sus scrofa connective tissue growth factor (CTGF) mRNA, complete
DEFINITION cds.
ACCESSION U83916
VERSION U83916.1 GI:2317891
KEYWORDS
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 1496)
AUTHORS Brigstock,D.R., Steffen,C.L., Kim,G.Y., Vegunta,R.K., Diehl,J.R.
and Harding,P.A.
TITLE Purification and characterization of novel heparin-binding growth
factors in uterine secretory fluids. Identification as
heparin-regulated Mr 10,000 forms of connective tissue growth
factor
JOURNAL J. Biol. Chem. 272 (32), 20275-20282 (1997)
MEDLINE 97390475
REFERENCE 2 (bases 1 to 1496)
AUTHORS Harding,P.A. and Brigstock,D.R.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-1997) Surgery, Children's Hospital, 700
Children's Drive, Columbus, OH 43205, USA
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QY 61 ctggtccagaccacagatggagcgcctgttccaagacctgtggatgggcatctccacc 120
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[illegible]



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241 cccaaatctccaaagcctcattcaagtttgccttctgctgctgacccagcagatgaagacatc 300

934 CCAAAAATCTCAAGCCCATCAAGTTTGGCTGTGGCTGACCCAGCGTGAAGACGTAC 993

301 cgaactaaattctgtgagttatgtaccagacggcgagctgctgacccccccacagaccacc 360

994 AGAGTAAATCTGTGGTGTCTGCACCTGACGGGGCTGTGCACACCCCCACAGACAGCC 1053

361 accctgcccgtgagttcgaagtcacgtgcccctgacggcgaggtcatgaagaacatgatgttc 420

1054 ACCCTCCCGTGGAGTTCAAGTCCCGGATGAGAGATCATGAAGAGGAAATGATGTTTC 1113

421 atcaagacctgtgctgacattacacgttcccgagacatgacatgacatctttgtaacgtcg 480

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1174 TACTACAGGAAGATGTATGGAGACATGGCA 1203

RESULT 15

NV1271167 1585 bp mRNA VRT 14-JAN-2000

LOCUS Notophthalmus viridescens mRNA for connective tissue growth factor

DEFINITION (ctgf, gene).

ACCESSION AJ271167.1 GI:6706300

VERSION connective tissue growth factor; CTGF gene.

KEYWORDS eastern newt.

SOURCE Notophthalmus viridescens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Caudata; Salamandridae; Notophthalmus.

REFERENCE 1 (bases 1 to 1585)

Cash, D.E., Gates, P.B., Imokawa, Y. and Brookes, J.P.

Identification of new connective tissue growth factor as a target

of retinoid regulation in limb blastemal cells

Gene 222 (1), 119-124 (1998)

JOURNAL MEDLINE 99033008

REFERENCE 2 (bases 1 to 1585)

Gates, P.B.

Direct Submission

Submitted (11-JAN-2000) Gates P.B., Biochemistry, University

College London, Gower Street London, WC1E 6BT, UNITED KINGDOM

Location/Qualifiers

1. 1585

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/db\_xref="taxon:8316"

/country="USA"

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BASE COUNT

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Matches 440; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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DB 568 GCTGTGTACAGACAGAGAAACCTATGGCGCGGATCTTCCTTGATGCTGCGCAACTGC 727  
QY 61 ctgggtccagaccacagagtggagcctgttccaaagacctgtgggagtggtggtccacc 120  
DB 728 CTGGTCCAGACTACGGAATGGAGTGGCTGCTCGAAGACATGGCGCATGGGCATCTCCACC 787  
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QY 181 aggccttgcaagctgacctggaagaaacattaaagagggaagaaagtgcctccgtact 240  
DB 848 AGACCTGTGAGGCACACCTGGAGGAGACATTAAGAAAGGCAAGAGTGCATTCGTACC 907  
QY 241 cccaaatctccaagcctatcaagtttgagcttcttggtgcaccagcatgaagacatac 300  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2001, 21:25:44 ; Search time 127.58 Seconds  
(without alignments)  
2510.032 Million cell updates/sec

Title: US-09-461-646-1\_COPY\_667\_1176

Perfect score: 510

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510	100.0	1415	21	AA11281 Human connective t
2	510	100.0	2075	16	AAT04226 Connective tissue
3	510	100.0	2075	18	AAT45360 Human connective t
4	510	100.0	2075	18	AAT51234 Connective tissue
5	510	100.0	2075	19	AAV38085 Human connective t
6	510	100.0	2075	20	AAV61317 Human connective t
7	510	100.0	2075	21	AA11278 Human connective t
8	510	100.0	2075	21	AA11280 Human connective t
9	510	100.0	2075	22	AAF59354 Human connective t
10	510	100.0	2075	22	AAC87517 Human connective t
11	433.8	85.1	2267	18	AAT94700 Murine Fisp12 cDNA

12	433.8	85.1	2330	13	AAQ26422	Gene for beta-IG-M
13	433.8	85.1	2338	20	AAV90030	Rat connective tis
14	427.4	83.8	2350	21	AA115477	Clone 2-4-7 encodi
15	299.4	58.7	2553	21	AAV78039	Human cancer assoc
16	296.4	58.1	4212	20	AAV65380	Connective tissue
17	296.4	58.1	4214	18	AAT59618	Connective tissue
18	296.4	58.1	4214	18	AAT58534	Human connective t
19	287.2	56.3	486	22	AAF22294	Bovine mammary tis
20	286.4	56.2	488	20	AAV29126	Poly nucleotide RFP
21	283.4	55.6	341	21	AAV50437	Mouse connective t
22	280.2	54.9	341	21	AAV50436	Mouse connective t
23	180	35.3	1975	14	AAQ36031	Rat connective tis
24	157.2	30.8	1146	18	AAT97142	Chicken nov coding
25	157.2	30.8	1418	18	AAV94699	Human monocyte mat
26	157.2	30.8	2270	21	AAV98875	Human cysteine ric
27	157.2	30.8	2270	21	AAV98157	Human proliferatio
28	157.2	30.8	2307	21	AAV78196	Human cancer assoc
29	155.6	30.5	1128	17	AAT12553	Connective tissue
30	153	30.0	1128	20	AAV11720	Human CTGF-2 cDNA
31	150.8	29.6	2028	13	AAQ26421	Gene for beta-IG-M
32	144.8	28.4	1062	20	AAV11246	Human connective t
33	135	26.5	1101	20	AAV76483	Human WISP-1 prote
34	135	26.5	1140	20	AAV76485	Mouse WISP-1 prote
35	135	26.5	1183	20	AAV76494	Human WISP-1 clone
36	135	26.5	1403	20	AAV76490	Human WISP-1 clone
37	135	26.5	1766	20	AAV76484	Mouse WISP-1 prote
38	135	26.5	2795	22	AAV91577	Human PRO342 cDNA
39	135	26.5	3658	21	AAV58613	Human connective t
40	133.4	26.2	2830	20	AAV76482	Human WISP-1 prote
41	129.4	25.4	619	14	AAQ36046	Human sequence XXV
42	122	23.9	546	20	AAV76495	Human WISP-1 clone
43	122	23.9	683	20	AAV76492	Human WISP-1 clone
44	119.2	23.4	1142	20	AAV11245	Human connective t
45	119.2	23.4	1183	21	AAV06928	Human growth facto

#### ALIGNMENTS

RESULT 1  
AA11281  
ID AA11281 standard; cDNA; 1415 BP.  
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AC AA11281;  
XX  
DT 08-NOV-2000 (first entry)  
XX  
DE Human connective tissue growth factor partial cDNA.  
XX  
KW Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;  
KW fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;  
KW hypertrophic scarring; atherosclerosis; diabetic nephropathy; retinopathy;  
KW hypertension; cardiovascular disorder; wound healing; bone repair; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200035939-A2.  
XX  
PD 22-JUN-2000.  
XX  
PF 14-DEC-1999; 99WO-US29654.  
XX  
PR 14-DEC-1998; 98US-0112240.  
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PR 14-DEC-1998; 98US-0112241.  
XX  
PA (UYMI-) UNIV MIAMI.  
XX  
PA (FIBR-) FIBROGEN INC.  
XX  
PI Grotendorst GR, Neff TB;  
XX  
XX  
DR WPI; 2000-431568/37.  
XX  
DR P-PSDB; AAV92941.  
XX

Tue Aug 21 08:16:51 2001

Connective tissue growth factor; CTGF; wound healing; vulnary;  
cell proliferation; cancer; fibrosis; atherosclerosis; diagnosis  
therapy; mitogen; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 130..1179  
/tag= a

US5408040-A.

18-APR-1995.

30-AUG-1991; 91US-0752427.

30-AUG-1991; 91US-0752427.

14-DEC-1993; 93US-0167628.

(UYSF-) UNIV SOUTH FLORIDA.

Bradham DM, Grotendorst GR;

WPI; 1995-161147/21.

P-PSDB; AAR79964.

New connective tissue growth factor - used to develop prods. for wound healing and for diagnosis and therapy of cell proliferative disorders.

Example 5; Column 15-18; 12pp; English.

A cDNA clone (AAT04226), designated DB60R32, codes for human connective tissue growth factor (CTGF) (AAR79964), a protein that has mitogenic and chemotactic activity for connective tissue cells and which binds to the platelet-derived growth factor (PDGF) receptor. The cDNA was obtained from a library of human umbilical vein endothelial cell cDNA in vector lambda gt11 by screening with an anti-PDGF antibody. The cDNA is useful for prodn. of recombinant CTGF or in the design of antisense or ribozyme constructs used to treat disorders associated with overgrowth of tissue cells, such as cancer, fibrotic diseases and atherosclerosis.

Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;

Query Match 100.0%; Score 510; DB 16; Length 2075;

Best Local Similarity 100.0%; Pred. No. 1.1e-144; Indels 0; Gaps 0;

Matches 510; Conservative 0; Mismatches 0;

1 gcggcttacgactggaagacacgcttggccagacaccccaactatgattagagccaactgc 60

667 gcggcttacgactggaagacacgcttggccagacaccccaactatgattagagccaactgc 726

61 ctggtccagacacagagtgagcgcctgttccaaagacctgtggatgggcatctccacc 120

727 ctggtccagacacagagtgagcgcctgttccaaagacctgtggatgggcatctccacc 786

121 cgggttaccatgatcaacgctcctcagctagagagagcagagccgctgtgcatggtc 180

787 cgggttaccatgatcaacgctcctcagctagagagagcagagccgctgtgcatggtc 846

181 aggccttcgaaagctgacctggaagagacacattagaggggcaaaagtgcattccctact 240

847 aggccttcgaaagctgacctggaagagacacattagaggggcaaaagtgcattccctact 906

241 cccaaatctccaaagcctatcaagtttgagcttttggctgaccagcatgaagacatc 300

907 cccaaatctccaaagcctatcaagtttgagcttttggctgaccagcatgaagacatc 966

301 cgagctaaattctgttgagtagtaccgagcgcctgctgaccccccacagacacc 360

Qy

New fragment of connective tissue growth factor (CTGF) polypeptide  
having mitogenic activity, useful in wound healing, bone and tissue  
repair

Disclosure: Fig 3; 7lpp; English.

This sequence represents a partial coding sequence for the human connective-tissue growth factor (CTGF) polypeptide which has mitogenic activity. The sequence spans the open reading frame covering exons 2 and 3 of the full length sequence (AAL1280). The protein can be used to treat a raise antibodies which specifically bind to CTGF and are used to treat a CTGF-associated disease or disorder, e.g. a fibroproliferative disease/disorder such as kidney fibrosis, scleroderma, pulmonary disease, liver fibrosis, arthritis, hypertrophic scarring, fibrosis, liver fibrosis, arthrits, hyperinflation, hypertension, atherosclerosis, diabetic nephropathy and retinopathy, skin fibrotic kidney disorders, angioneuromatosis-related disorders, skin fibrotic disorders, and cardiovascular disorders. The protein is also useful in wound healing, bone and tissue repair.

Sequence 1415 BP; 403 A; 299 C; 329 G; 384 T; 0 other;

Query Match 100.0%; Score 510; DB 21; Length 1415;

Best Local Similarity 100.0%; Pred. No. 8.9e-145; Indels 0; Gaps 0;

Matches 510; Conservative 0; Mismatches 0;

1 gcggcttacgactggaagacacgcttggccagacaccccaactatgattagagccaactgc 60

7 gcggcttacgactggaagacacgcttggccagacaccccaactatgattagagccaactgc 66

61 ctggtccagacacagagtgagcgcctgttccaaagacctgtggatgggcatctccacc 120

67 ctggtccagacacagagtgagcgcctgttccaaagacctgtggatgggcatctccacc 126

121 cgggttaccatgatcaacgctcctcagctagagagagcagagccgctgtgcatggtc 180

127 cgggttaccatgatcaacgctcctcagctagagagagcagagccgctgtgcatggtc 186

181 aggccttcgaaagctgacctggaagagacacattagaggggcaaaagtgcattccctact 240

187 aggccttcgaaagctgacctggaagagacacattagaggggcaaaagtgcattccctact 246

241 cccaaatctccaaagcctatcaagtttgagcttttggctgaccagcatgaagacatc 300

247 cccaaatctccaaagcctatcaagtttgagcttttggctgaccagcatgaagacatc 306

301 cgagctaaattctgttgagtagtaccgagcgcctgctgaccccccacagacacc 360

307 cgagctaaattctgttgagtagtaccgagcgcctgctgaccccccacagacacc 366

361 acctgcgggtgagttcaagtgcctgacgagcagcaggtcatgaagaacatgatgttc 420

367 acctgcgggtgagttcaagtgcctgacgagcagcaggtcatgaagaacatgatgttc 426

421 atcaagacctgtgctgcctatcaactgtcccgagacatgacatctttgcatcgtg 480

427 atcaagacctgtgctgcctatcaactgtcccgagacatgacatctttgcatcgtg 486

481 tactacaggaagatgtacgagacatggca 510

487 tactacaggaagatgtacgagacatggca 516

RESULT 2

AAT04226

ID AAT04226 standard; cDNA; 2075 BP.

XX AAT04226;

XX 12-JUN-1996 (first entry)

XX Connective tissue growth factor cDNA.

XX

Db 967 cgagctaaattctgtgagtatgtacagacggcgcgatctgcaacccccacagaaccacc 1026  
 QY 361 accctgcgggtgagttcaagtccctgacggcgaggtcatgaagaacaacatgatcttc 420  
 Db 1027 accctgcgggtgagttcaagtccctgacggcgaggtcatgaagaacaacatgatcttc 1086  
 QY 421 atcaagacctgtgcctgacctatacaactgtcccgagagacaatgacatctttgaaatgcctg 480  
 Db 1087 atcaagacctgtgcctgacctatacaactgtcccgagagacaatgacatctttgaaatgcctg 1146  
 QY 481 tactacaggaagatgtacggagacatggca 510  
 Db 1147 tactacaggaagatgtacggagacatggca 1176

RESULT 3  
 AAT45360  
 ID AAT45360 standard; cDNA; 2075 BP.  
 XX  
 AC AAT45360;  
 XX  
 DT 26-APR-1997 (first entry)  
 XX  
 DE Human connective tissue growth factor cDNA.  
 XX  
 KW Connective tissue growth factor; CTGF; mitogen; cell proliferation;  
 KW wound healing; cancer; tumor; fibrosis; glaucoma; atherosclerosis;  
 KW diagnosis; therapy; antisense; triple helix; ribozyme; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 130..1179  
 FT /\*tag= a  
 XX  
 PN W09638172-A1.  
 XX  
 XX 05-DEC-1996.  
 XX  
 XX 31-MAY-1996; 96WO-0508140.  
 XX  
 PR 31-MAY-1996; 96WO-0508140.  
 XX  
 PA (UYSF-) UNIV SOUTH FLORIDA.  
 XX  
 PI Bradham DM, Grotendorst GR;  
 XX  
 XX WPI; 1997-042659/04.  
 DR P-PSDB; AAW09089.  
 XX  
 XX Connective tissue growth factor coding sequence and protein - used  
 PT in the treatment of proliferative disorders and to accelerate wound  
 PT healing  
 XX  
 PS Clalm 20; Page 50-52; 76pp; English.  
 XX  
 CC A cDNA clone (AAT45360) codes for novel human connective tissue growth  
 CC factor (CTGF) (AAW09089), a PDGF-immunorelated protein that may play a  
 CC significant role in the normal development, growth and repair of  
 CC human tissue and which probably functions as a growth factor in  
 CC wound healing. CTGF may be involved in diseases in which there is  
 CC an overgrowth of connective tissue cells, such as cancer, tumor  
 CC formation and growth, fibrotic diseases (e.g. pulmonary fibrosis,  
 CC kidney fibrosis, glaucoma) and atherosclerosis. The cDNA clone was  
 CC isolated from a HUVEC cDNA library using anti-PDGF antibody. CTGF  
 CC nucleic acids can be used for recombinant prodn. of CTGF and as  
 CC probes to detect CTGF mRNA. CTGF genomic DNA (AAT58534) has also  
 CC been isolated. A proliferative disorder may be treated using e.g.  
 CC a CTGF antisense, ribozyme or triplex agent.  
 XX  
 SI Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;

Query Match 100.0%; Score 510; DB 18; Length 2075;  
 Best Local Similarity 100.0%; Pred. No. 1..1e-144;  
 Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 gcggcttacgcagactggaagacacagctgttggcccgagaccacactatgattagagcaactgc 60  
 Db 667 gcggcttacgcagactggaagacacagctgttggcccgagaccacactatgattagagcaactgc 726  
 QY 61 ctggtccagaccacagagtgagcgctgttccaagacctgtgggagtgatccatccacc 120  
 Db 727 ctggtccagaccacagagtgagcgctgttccaagacctgtgggagtgatccatccacc 786  
 QY 121 cgggttaccatgacacgcctcctcaggtctagagagcagagcccgctgtgcattgctc 180  
 Db 787 cgggttaccatgacacgcctcctcaggtctagagagcagagcccgctgtgcattgctc 846  
 QY 181 aggccttgcaagctgacctggaagaaacattaaagggcgaagaaagtgcattcctact 240  
 Db 847 aggccttgcaagctgacctggaagaaacattaaagggcgaagaaagtgcattcctact 906  
 QY 241 cccaaaatctccaaagcctatacaagtttgagctttctgctgcaccagcatgaagacatac 300  
 Db 907 cccaaaatctccaaagcctatacaagtttgagctttctgctgcaccagcatgaagacatac 966  
 QY 301 cgagctaaattctgtgagtgatgtaccgacggcgctgctgcaccccccacagaaacacc 360  
 Db 967 cgagctaaattctgtgagtgatgtaccgacggcgctgctgcaccccccacagaaacacc 1026  
 QY 361 acctgcgggtgagttcaagtgccctgacggcgaggtctatgaagaagaacatgatgttc 420  
 Db 1027 acctgcgggtgagttcaagtgccctgacggcgaggtctatgaagaagaacatgatgttc 1086  
 QY 421 atcaagacctgtgctgctccattacaactgtcccgagagacaatgacatctttgaatcctg 480  
 Db 1087 atcaagacctgtgctgctccattacaactgtcccgagagacaatgacatctttgaatcctg 1146  
 QY 481 tactacaggaagatgtacggagacatggca 510  
 Db 1147 tactacaggaagatgtacggagacatggca 1176

RESULT 4  
 AAT51234  
 ID AAT51234 standard; cDNA; 2075 BP.  
 XX  
 AC AAT51234;  
 XX  
 DT 18-MAR-1997 (first entry)  
 XX  
 DE Connective tissue growth factor coding sequence.  
 XX  
 KW Connective tissue growth factor; CTGF; human; connective tissue cell;  
 KW proliferative disease; platelet-derived growth factor; PDGF; development;  
 KW tissue growth; repair; umbilical vein endothelial cell; HUVE cell;  
 KW antibody; wound healing; cancer; fibrotic disease; atherosclerosis;  
 KW inhibitor; protease degradation; growth factor; therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 130..1179  
 FT /\*tag= a  
 FT /product= connective tissue growth factor  
 XX  
 PN US5585270-A.  
 XX  
 XX 17-DEC-1996.  
 PD  
 XX 30-AUG-1991; 91US-0752427.  
 PF  
 XX 30-AUG-1991; 91US-0752427.  
 PR 14-DEC-1993; 93US-0167628.  
 PR 10-FEB-1995; 95US-0386680.

•

Query Match	100.0%	Score	510:	DB	18:	Length	2075:
Best Local Similarity	100.0%	Pred. No.	1.1e-144:	Indels	0:	Gaps	0
Matches	510:	Conservative	0:	Mismatches	0:		
Y	1	gcgggtaccgactcggagacacgcttggccagagcccaactatgattagagccaactgc	60				
b	667	gcgggtaccgactcggagacacgcttggccagagcccaactatgattagagccaactgc	726				
Y	61	ctgtgtccagaccacagatggagcgcctgttccaagacctgtggatgggcatctccacc	120				
b	727	ctgtgtccagaccacagatggagcgcctgttccaagacctgtggatgggcatctccacc	786				
Y	121	cgggttaccaatgacacccctctctgcaggtctagaagcagagcgcctgtgcattggctc	846				
b	787	cgggttaccaatgacacccctctctgcaggtctagaagcagagcgcctgtgcattggctc	240				
Y	181	aggcctgcgaagctgacctggaagagaaacattaaagaaggccaaagtgcattccgtact	906				
b	847	aggcctgcgaagctgacctggaagagaaacattaaagaaggccaaagtgcattccgtact	300				
Y	241	cccaaatctccaagcctatcaagtttgaccttctggctgcaccagcatgaagacatac	966				
b	907	cccaaatctccaagcctatcaagtttgaccttctggctgcaccagcatgaagacatac	360				
Y	301	cgagctcaaatctgtggagtagtaccagagcccgatgtgcaccctccacagaccacc	1026				
b	967	cgagctcaaatctgtggagtagtaccagagcccgatgtgcaccctccacagaccacc	420				
Y	361	acctgcgggtgagttcgaagtgcacctgacggcgaggtcatgatgaagacaatgatgttc	1086				
b	1027	acctgcgggtgagttcgaagtgcacctgacggcgaggtcatgatgaagacaatgatgttc	480				
Y	421	atcaagacctgtgcctgccaattacaactgtcccggagacaatgacattcttgaatgcgtg	1146				
b	1087	atcaagacctgtgcctgccaattacaactgtcccggagacaatgacattcttgaatgcgtg					
Y	481	tactacaggaagatgtacggagacatggca	510				

```

RESULT      5
AAV38085 standard; cDNA; 2075 BP.
ID          AAV38085;
XX          AAV38085;
AC          AAV38085;
XX          15-SEP-1998 (first entry)
DT          Human connective tissue growth factor encoding cDNA.
XX          Human connective tissue growth factor; CTGF; PDGF; diagnosis; cancer;
DE          Human; connective tissue growth factor; ameliorating cell proliferative disorder;
XX          platelet derived growth factor; ameliorating cell proliferative disorder;
KW          atherosclerosis; fibrotic disease; ss.
XX          Homo sapiens.
OS          Location/Qualifiers
FH          Key               130..1179
FT          CDS              /*tag= a
                             /product= "connective tissue growth factor"
XX          US5783187-A.
XX          21-JUL-1998.
PD          11-SEP-1996;    96US-0712302.
PF          30-AUG-1991;    91US-0752427.
PR          14-DEC-1993;    93US-0167628.
PP          11-SEP-1996;    96US-0712302.
XX          (UYSF-) UNIV SOUTH FLORIDA.
PA          Bradham DM, Grotendorst GR;
XX          WPI; 1998-426958/36.
PI          P-PSDB; AAW62084.
XX          Ameliorating cell proliferative disorder associated with connective
PT          tissue growth factor - comprises the administration of an antibody
PT          which binds to connective tissue growth factor and not to
PT          platelet-derived growth factor
XX          Example 6; Column 15-18; lipp; English.
PS          A method has been developed for ameliorating a cell proliferative
CC          disorder associated with connective tissue growth factor (CTGF). The
CC          method comprises the administration of an antibody or its fragment that
CC          binds to CTGF and not to platelet-derived growth factor (PDGF), to the
CC          site of the disorder. CTGF is related immunologically and biologically
CC          to PDGF. The present sequence encodes CTGF. The method is used to treat
CC          conditions involving the overgrowth of connective tissue cells such
CC          as cancer, atherosclerosis and other fibrotic diseases.
XX          Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;
XX          Query Match           100.0%; Score 510; DB 19; Length 2075;
XX          Best Local Similarity 100.0%; Pred. No. 1.1e-144;
XX          Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps
QY          1 cgcgcttacgcactggaagacacgtttggccagaccaccaactgattgaggccaactgc 60
Db          |
QY          667 gggcgttaccgcactgggaagacgtttggccagaccaccaactgattgaggccaactgc 726
Db          |
QY          61 ctgggttcagaccacagatggagcgctgttccaaagacctgtgggatggcatctccacc 120
Db          |
QY          727 ctgggttcagaccacagatggagcgctgttccaaagacctgtgggatggcatctccacc 786
Db          |
QY          121 cgsgttaccatgaacaacgcctctgcaggctagagaagacagacgcgcctgtgcattgc 180

```

Db 787 cgggttaccgaatgacacgctcctctgagctagagaagcagcgcctgtgctggtc 846  
 Qy 181 agccttgcgaagctgacctggaagagacattaaagagggcgaagagtgatccctgact 240  
 Db 847 agccttgcgaagctgacctggaagagacattaaagagggcgaagagtgatccctgact 906  
 Qy 241 cccaaatctccaaagcctatcaagtgtgagcttctggtgcaccagcatgaagacatac 300  
 Db 907 cccaaatctccaaagcctatcaagtgtgagcttctggtgcaccagcatgaagacatac 966  
 Qy 301 cgaagctaaattctgtgagctatgtaccagcggccgagctgtgaccccccacagaaccac 360  
 Db 967 cgaagctaaattctgtgagctatgtaccagcggccgagctgtgaccccccacagaaccac 1026  
 Qy 361 accctgcgggtgaggttcaagtgcctgcgagcggaggttcattgaagaagacatgatttc 420  
 Db 1027 accctgcgggtgaggttcaagtgcctgcgagcggaggttcattgaagaagacatgatttc 1086  
 Qy 421 atcaagacctgtgcctgcctaccactgtcccgaggagacacatctttgaaatcgctg 480  
 Db 1087 atcaagacctgtgcctgcctaccactgtcccgaggagacacatctttgaaatcgctg 1146  
 Qy 481 tactacaggaagatgtacggagacatggca 510  
 Db 1147 tactacaggaagatgtacggagacatggca 1176

## RESULT 6

AA61317  
 ID AAX61317 standard; cDNA; 2075 BP.

XX AC AAX61317;

XX DT 20-AUG-1999 (first entry)

XX DE Human connective tissue growth factor coding sequence.

XX KW CTGF; connective tissue growth factor; human; fibrotic disease;

XX KW cell proliferative disorder; atherosclerosis; diagnosis; ss.

XX OS Homo sapiens.

XX XX US5916756-A.

XX PN 29-JUN-1999.

XX XX 20-JUN-1997; 97US-0880031.

XX PF 14-DEC-1993; 93US-0167628.

XX PR 10-FEB-1995; 95US-0386680.

XX PR 11-SEP-1996; 96US-0712302.

XX PR 20-JUN-1997; 97US-0880031.

XX XX (UYSF-) UNIV SOUTH FLORIDA.

XX PA Bradham DM, Grotendorst GR;

XX PI WPI: 1999-384720/32.

XX DR P-PSDB; AAY18361.

XX XX Detecting cell proliferative disorders such as fibrotic disease and

XX PT atherosclerosis

XX PS Disclosure; Column 15-18; l1pp; English.

XX XX This sequence encodes the human connective tissue growth factor (CTGF).

XX CC The invention relates to a method of detecting a cell proliferative

XX CC disorder comprising comparing the level of CTGF in a sample against a

XX CC control, where an increase is indicative of a cell proliferative disorder

XX CC (fibrotic disease or atherosclerosis). The method is used to detect cell

SQ Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;

Query Match 100.0%; Score 510; DB 20; Length 2075;

Best Local Similarity 100.0%; Pred. No. 1,1e-144;

Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcggttaccgactggaagacacgctttggccagaccccaactatgattagaccaactgc 60  
 Db 667 gcggttaccgactggaagacacgctttggccagaccccaactatgattagaccaactgc 726  
 Qy 61 ctggttcagaccacagagtgagcgcctgttccaaagacctgtgggagcattctccacc 120  
 Db 727 ctggttcagaccacagagtgagcgcctgttccaaagacctgtgggagcattctccacc 786  
 Qy 121 cgggtttaccaaatgacaacgcctctcagcttagaagacagagccgcctgtgcatggtc 180  
 Db 787 cgggtttaccaaatgacaacgcctctcagcttagaagacagagccgcctgtgcatggtc 846  
 Qy 181 agccttgcgaagctgacctggaagagacattaaagagggcgaagagtgatccctgact 240  
 Db 847 agccttgcgaagctgacctggaagagacattaaagagggcgaagagtgatccctgact 906  
 Qy 241 cccaaatctccaaagcctatcaagtgtgagcttctggtgcaccagcatgaagacatac 300  
 Db 907 cccaaatctccaaagcctatcaagtgtgagcttctggtgcaccagcatgaagacatac 966  
 Qy 301 cgaagctaaattctgtgagctatgtaccagcggccgagctgtgaccccccacagaaccac 360  
 Db 967 cgaagctaaattctgtgagctatgtaccagcggccgagctgtgaccccccacagaaccac 1026  
 Qy 361 accctgcgggtgaggttcaagtgcctgcgagcggaggttcattgaagaagacatgatttc 420  
 Db 1027 accctgcgggtgaggttcaagtgcctgcgagcggaggttcattgaagaagacatgatttc 1086  
 Qy 421 atcaagacctgtgcctgcctaccactgtcccgaggagacacatctttgaaatcgctg 480  
 Db 1087 atcaagacctgtgcctgcctaccactgtcccgaggagacacatctttgaaatcgctg 1146  
 Qy 481 tactacaggaagatgtacggagacatggca 510  
 Db 1147 tactacaggaagatgtacggagacatggca 1176

## RESULT 7

AA611278  
 ID AA611278 standard; cDNA; 2075 BP.

XX AC AA611278;

XX DT 08-NOV-2000 (first entry)

XX DE Human connective tissue growth factor cDNA.

XX KW Dermatological; antiarthritic; antiarteriosclerotic; antidiabetic;  
 KW nephrotropic; ophthalmological; hypotensive; cardiac; tranquilizer;  
 KW vulnary; antiinflammatory; human; connective tissue growth factor;  
 KW CTGF; extracellular matrix synthesis; collagen synthesis; antibody;  
 KW myofibroblast differentiation; antisense; fibroproliferative disease;  
 KW fibrosis; trauma; cancer; inflammation; diabetes; keloid; ss.

XX OS Homo sapiens.

XX XX WO200035936-A1.

XX PN 22-JUN-2000.

XX XX 14-DEC-1999; 99WO-US29652.

XX XX 14-DEC-1998; 98US-0112240.

XX PR 14-DEC-1998; 98US-0112241.

XX XX (UYMI-) UNIV MIAMI.





Db 727 ctggtccagaccacagagtgagcgctgtccaaagacctgtggagcattctccacc 786  
QY 121 cgggttaccacagacacccctcctcagcctagagaagcagcgccctgtgcatggtc 180  
Db 787 cgggttaccacagacacccctcctcagcctagagaagcagcgccctgtgcatggtc 846  
QY 181 aggccttgcgaagctgacctggaagagacattaaagaaggcgaagagtgatccgtact 240  
Db 847 aggccttgcgaagctgacctggaagagacattaaagaaggcgaagagtgatccgtact 906  
QY 241 cccaaatctccaaagcctatcaagtttgagcttcttgcctgacccagcatgaagacatac 300  
Db 907 cccaaatctccaaagcctatcaagtttgagcttcttgcctgacccagcatgaagacatac 966  
QY 301 cgaagctaaattctgtgagatgtatgacagcagcgccgagctgctgaccccccacagaccacc 360  
Db 967 cgaagctaaattctgtgagatgtatgacagcagcgccgagctgctgaccccccacagaccacc 1026  
QY 361 accctgcgggtgagttcaagtgcctgacgagcgaggttcagagagacatgatgttc 420  
Db 1027 accctgcgggtgagttcaagtgcctgacgagcgaggttcagagagacatgatgttc 1086  
QY 421 atcaagacctgtgctgctccattacaactgtcccgagagacaaatgacatctttgaaatcgctg 480  
Db 1087 atcaagacctgtgctgctccattacaactgtcccgagagacaaatgacatctttgaaatcgctg 1146  
QY 481 tactacaggaagatgtacggagacatggcca 510  
Db 1147 tactacaggaagatgtacggagacatggcca 1176

## RESULT 9

AAF59954  
ID AAF59954 standard; cDNA; 2075 BP.

XX AAF59954;  
XX  
XX  
XX 22-MAY-2001 (first entry)  
XX Human connective tissue growth factor (CTGF) cDNA.  
XX Human CTGF; connective tissue growth factor; recombinant production;  
KW mitogenic; chemotactic; tissue development; growth; repair;  
KW wound healing; vulnary; diagnostic agent;  
KW cellular proliferation disorder; ss.  
XX  
XX Homo sapiens.  
XX  
XX US6190884-B1.  
XX  
XX 20-FEB-2001.  
XX  
XX 18-MAY-1998; 98US-0080715.  
XX  
XX 14-DEC-1993; 93US-0167628.  
PR 10-FEB-1995; 95US-0386680.  
PR 30-AUG-1991; 91US-0752427.  
PR 11-SEP-1996; 96US-0712302.  
XX  
XX (UYSF-) UNIV SOUTH FLORIDA.  
XX  
XX Grotendorst GR, Bradham DM;  
XX  
XX WPI: 2001-210379/21.  
DR P-PSDB; AAB60664.  
XX  
XX Producing connective tissue growth factor involves transforming a host  
PT cell with polynucleotide encoding the growth factor and growing the  
PT cell under optimum conditions so that the polynucleotide is expressed  
PT  
XX  
PS Claim 9; Column 15-18; 11pp; English.

XX The invention relates to a method for the recombinant production of  
CC human connective tissue growth factor (CTGF; AAB60664), involving  
CC transforming a prokaryotic or eukaryotic host cell with an expression  
CC construct comprising the CTGF cDNA sequence (AAF59954) or a fragment  
CC thereof, and culturing the host cell under conditions suitable for the  
CC expression of CTGF. CTGF is a mitogen and chemotactic agent for  
CC connective tissue cells and plays a significant role in normal  
CC development, growth and repair of human tissues. It is useful as a  
CC therapeutic for accelerating wound healing and promoting normal healing  
CC mechanisms and may therefore be used in the treatment of e.g., burns.  
CC CTGF is also useful as a diagnostic reagent for diagnosing pathological  
CC states in a patient suspected of having a disease characterised by a  
CC disorder of cellular proliferation. The present sequence represents  
CC cDNA encoding human CTGF.  
XX  
SQ Sequence 2075 BP; 491 A; 558 C; 546 G; 480 T; 0 other;

Query Match 100.0%; Score 510; DB 22; Length 2075;  
Best Local Similarity 100.0%; Pred NO. 1,1e-144;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggttaccgactggaagacacgtttggccagaccacaaactatgattagaccaactgc 60  
Db 667 gcggttaccgactggaagacacgtttggccagaccacaaactatgattagaccaactgc 726  
QY 61 ctggtccagaccacagagtgagcgctgttccaaagacctgtgggagcattctccacc 120  
Db 727 ctggtccagaccacagagtgagcgctgttccaaagacctgtgggagcattctccacc 786  
QY 121 cgggttaccacatgacacgcctcctcagctagagaagcagagccgctgtgcatggtc 180  
Db 787 cgggttaccacatgacacgcctcctcagctagagaagcagagccgctgtgcatggtc 846  
QY 181 aggccttgcgaagctgacctggaagagacattaaagaaggcgaagagtgatcccgctact 240  
Db 847 aggccttgcgaagctgacctggaagagacattaaagaaggcgaagagtgatcccgctact 906  
QY 241 cccaaatctccaaagcctatcaagtttgagcttcttgcctgacccagcatgaagacatac 300  
Db 907 cccaaatctccaaagcctatcaagtttgagcttcttgcctgacccagcatgaagacatac 966  
QY 301 cgaagctaaattctgtgagatgtatgacgagcgctgctgaccccccacagaccacc 360  
Db 967 cgaagctaaattctgtgagatgtatgacgagcgctgctgaccccccacagaccacc 1026  
QY 361 accctgcgggtgagttcaagtgcctcagcgagcgaggttcagagaagaacatgatgttc 420  
Db 1027 accctgcgggtgagttcaagtgcctcagcgagcgaggttcagagaagaacatgatgttc 1086  
QY 421 atcaagacctgtgctgctccattacaactgtcccgagagacaaatgacatctttgaaatcgctg 480  
Db 1087 atcaagacctgtgctgctccattacaactgtcccgagagacaaatgacatctttgaaatcgctg 1146  
QY 481 tactacaggaagatgtacggagacatggcca 510  
Db 1147 tactacaggaagatgtacggagacatggcca 1176

## RESULT 10

AAC87517  
ID AAC87517 standard; cDNA; 2075 BP.

XX AAC87517;  
XX  
XX 09-MAR-2001 (first entry)  
XX Human connective tissue growth factor (CTGF) cDNA.  
XX Human; connective tissue growth factor; CTGF; PDGF-like activity;  
KW platelet-derived growth factor; transforming growth factor-beta;  
KW TGF-beta; mitogenic; proliferative; chemotactic; wound healing;









us-09-461-646-1\_copy\_667\_1176.rng

Tue Aug 21 08:16:51 2001

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2001, 21:26:19 ; Search time 80.25 Seconds  
(without alignments)  
1203.099 Million cell updates/sec

Title: US-09-461-646-1\_COPY\_667\_1176

Perfect score: 510

Sequence: 1 gcgcctaccactggaaga.....agatgtacggagacatggca 510

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9455562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq.\*

2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq.\*

3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq.\*

4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq.\*

5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510	100.0	2075	1	US-08-167-628-1
2	510	100.0	2075	1	US-08-386-680-1
3	510	100.0	2075	1	US-08-459-717-1
4	510	100.0	2075	1	US-08-712-302-1
5	510	100.0	2075	2	US-08-880-031-1
6	510	100.0	2075	3	US-09-097-179-1
7	510	100.0	2075	4	US-09-080-715-1
8	510	100.0	2075	5	PCT-US96-08140-1
9	510	100.0	2998	3	US-09-054-368-1
10	510	100.0	2998	3	US-09-054-274-1
11	510	100.0	2998	4	US-09-056-704-1
12	154	30.2	1128	2	US-08-459-101A-1
13	36	7.1	1158	3	US-08-844-188-45
14	34.2	6.7	293	3	US-08-866-340-13
15	34.2	6.7	293	3	US-09-103-875-17
16	33.2	6.1	15202	3	US-08-922-635-21
17	31	6.1	9757	1	US-08-093-453B-1
18	31	6.1	9759	1	US-08-459-041A-1
19	31	6.1	9759	3	US-08-999-733-1
20	30.8	6.0	1176	2	US-08-387-942C-17
21	30.8	6.0	12588	2	US-08-387-942C-1
22	30.8	6.0	28958	1	US-08-258-261B-6
23	30.8	6.0	28958	1	US-08-456-837-6
24	30.8	6.0	28958	1	US-08-457-342-6
25	30.8	6.0	28958	1	US-08-457-646A-6
26	30.8	6.0	28958	1	US-08-458-076A-6
27	30.8	6.0	28958	1	US-08-764-233A-4

## ALIGNMENTS

RESULT 1

US-08-167-628-1

; Sequence 1, Application US/08167628

; Patent No. 5408040

; GENERAL INFORMATION:

; APPLICANT: Grotendorst, Gary R.

; APPLICANT: Bradham Jr., Douglas M.,

; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Spensley Horn Jubas & Lubitz

; STREET: 4225 Executive Square, Suite 1400

; CITY: La Jolla

; STATE: CA

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/167,628

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/752,427

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Wetherell, Jr. Ph.D., John W.

; REGISTRATION NUMBER: 31,678

; REFERENCE/DOCKET NUMBER: PD-1294

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-455-5100

; TELEFAX: 619-455-5110

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2075 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; IMMEDIATE SOURCE:

; CLONE: DB60R32

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 130..1177

US-08-167-628-1

Sequence 6, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 1, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 1, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 3, Appl

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2
RESULT
US-08-386-680-1
: Sequence 1, Application US/08386680
: Patent No. 5585270
: GENERAL INFORMATION:
: APPLICANT: Grodenorst, Gary R.
: APPLICANT: Bradham Jr., Douglas M.,
: TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Spensley Horn Jubas. & Lubitz
: STREET: 4225 Executive Square, Suite 1400
: CITY: La Jolla
: STATE: CA
: COUNTRY: US
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/386.680
: FILING DATE: 10-FEB-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/167,628
: FILING DATE:
: APPLICATION NUMBER: US/07/752,427
: FILING DATE:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Wetherell, Jr. Ph.D., John W.

```



CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,717  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/752,427  
FILING DATE: 30-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr. Ph.D., John W.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-1294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-455-5100  
TELEFAX: 619-455-5110  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2075 base pairs  
TYPE: nucleic acid  
STRAINEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: DB60R32  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 130..1177  
US-08-459-717-1

Query Match 100.0%; Score 510; DB 1; Length 2075;  
Best Local Similarity 100.0%; Pred. No. 9,8e-139;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcttacgactggaagacacggtttggcccgagaccccaactatgattagagcaactgc 60  
Db 667 gcggcttacgactggaagacacggtttggcccgagaccccaactatgattagagcaactgc 726

QY 61 ctggtccagaccacagagtgagcctgttccaagacctgtggatggcactctccacc 120  
Db 727 CTGGTCCAGACCACAGAGTGAGCGGCTGTTCGAAGACCTGTGGGATGGGCACTCTCCACC 786

QY 121 cgggttaccgaatgacaaacgcctctcaggtctagagaagcagagccgctgtgcatggtc 180  
Db 787 CGGGTTACCAATGACAACGCCTCTCTGAGCTAGAGAAGCAGAGCCGCTGTGCATGCTC 846

QY 181 aggccttgcaagctgacctgggaagaaacattaaagaagggaagaaagtgcactc 240  
Db 847 AGGCCTTGGGAAGCTGACCTGGAAGAAACATTAAAGAAGGGCAAAAAGTGCATCCGTACT 906

QY 241 cccaaatctccaaagcctatcaagtttgagcttcttgctgacccagcagcatgaagacatc 300  
Db 907 CCCAAATCTCCAGGCTATCAAGTTTGAGCTTTCGGCTGACACGACATGAAGACATAC 966

QY 301 cgagctaaattctgtgagtatgtacacgagccgctgctgaccccccacacagaaaccac 360  
Db 967 CGAGCTAAATCTCTGGAGTATGTACGAGCGCGGATGTGACCCCGGATGTCACCCACCA 1026

QY 361 accctccgggtgaggttcaagtcacctgacggcgaggttcattgaagaagaacatgatttc 420  
Db 1027 ACCCTCCGGGTGAGGTTCAGAGTCCCTTGACGGGAGGTTCATGAAGAAGAACATGATGTC 1086

QY 421 atcaagacctgtgcctgacattacagactgtcccgagagacaataacatcttctgaatgcctg 480  
Db 1087 ATCAAGACCTGTGCCTGCCATTACAAGTGTCCCGGAGACAATGACATCTTTGAATCGCTG 1146

QY 481 tactacaggaagatgtacggagacatggca 510  
Db 1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176

RESULT 4  
US-08-712-302-1  
Sequence 1, Application US/08712302  
Patent No: 5783187  
GENERAL INFORMATION:  
APPLICANT: Grotendorst, Gary R.  
APPLICANT: Bradham Jr., Douglas M.,  
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/712,302  
FILING DATE: 11-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,680  
FILING DATE: 10-FEB-1995  
APPLICATION NUMBER: US/08/167,628  
FILING DATE:  
APPLICATION NUMBER: US/07/752,427  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Wetherell, Jr. Ph.D., John W.  
REGISTRATION NUMBER: 31,678  
REFERENCE/DOCKET NUMBER: PD-1294  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-455-5100  
TELEFAX: 619-455-5110  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2075 base pairs  
TYPE: nucleic acid  
STRAINEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: DB60R32  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 130..1177  
US-08-712-302-1

Query Match 100.0%; Score 510; DB 1; Length 2075;  
Best Local Similarity 100.0%; Pred. No. 9,8e-139;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcttacgactggaagacacggtttggcccgagaccccaactatgattagagcaactgc 60  
Db 667 gcggcttacgactggaagacacggtttggcccgagaccccaactatgattagagcaactgc 726

QY 61 ctggtccagaccacagagtgagcctgttccaagacctgtggatggcactctccacc 120  
Db 727 CTGGTCCAGACCACAGAGTGAGCGGCTGTTCGAAGACCTGTGGGATGGGCACTCTCCACC 786

QY 121 cgggttaccgaatgacaaacgcctctcaggtctagagaagcagagccgctgtgcatggtc 180

us-09-461-646-1-copy\_667\_1176.rni

Tue Aug 21 08:16:52 2001

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NAME/KEY: CDS
LOCATION: 130...1177
US-08-880-031-1

Query Match 100.0%; Score 510; DB 2; Length 2075;
Best Local Similarity 100.0%; Pred. No. 9,8e-139; Indels 0; Gaps 0;
Matches 510; Conservative 0; Mismatches 0;

1 gcggcttaccgactggaagacacgttttggcccgagaccacacattatgattagagccaactgc 60
667 GCGGCTTACCAGCTGGAAGACACGTTTGGCCCGACACCCACACCTATGATTAGAGCCCACTGC 726
61 ctgctccagaccagagtgaggagccctgttcccaagacctgtggtggtggtggtggtggtggt 120
61 ctgctccagaccagagtgaggagccctgttcccaagacctgtggtggtggtggtggtggtggt 786
727 CTGGTCCAGACACAGAGTGGAGCGCTGTTCAGAGACCTGTGGATGGGATGGGATGGGATGGG 180
121 cgggtaccagtggaacacgctcctcctcaggtcaggtcaggtcaggtcaggtcaggtcaggtc 846
787 CCGGTTTACCAGCTGGAAGACACGTTTGGCCCGACACCCACACCTATGATTAGAGCCCACTGC 240
181 aggccttgcgaagctgacgtggaagacacattaaagaggcgaagaggcgaagaggcgaagagg 300
847 AGGCTTGGAGAGCTGACCTGGAAGACACCTGGAAGACACCTGGAAGACACCTGGAAGACAC 966
241 cccaaatctccaaagcctcctcctcaggtcaggtcaggtcaggtcaggtcaggtcaggtcag 966
907 CCCAAATCTCCAAAGCCTATCAGTTTGGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTC 360
301 cgggtaccagtggaacacgctcctcctcaggtcaggtcaggtcaggtcaggtcaggtcaggtc 420
967 CGAGCTAAATCTCTGGAGTATGTACCGAGCGCGCGATGCTGACCGCGCGCGATGCTGACCG 1086
361 accctgcgggtgagttcaagtgcctcaggtcaggtcaggtcaggtcaggtcaggtcaggtcag 420
1027 ACCCTGCCGCTGGAGTTCAAGTGCCTGACGGCGAGGTCATGAGAGAGACATGATGTTTC 480
421 atcaagacctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1146
1087 ATCAAGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 510
481 tactacaggaagatgtacggagacatggca 510
1147 TACTACAGGAAGATGTACGGAGACATGGCA 1176

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RESULT 6
US-09-097-179-1
; Sequence 1, Application US/09097179
; Patent No. 6149916
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Juba & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/097,179
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2075 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: DB60R32
; FEATURE

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Query Match	100.0%	Score 510;	DB 4;	Length 2075;
Best Local Similarity	100.0%	Pred. No. 9.8e-139;		
Matches 510; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT 7  
US-09-080-715-1  
; Sequence 1, Application US/09080715  
; Patent No. 6190884  
; GENERAL INFORMATION:



QY 181 agccttggaagctgacctgggaaggaacattaaagaaggcgaaggaagtcacccgtact 240  
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Db 1742 agccttggaagctgacctgggaaggaacattaaagaaggcgaaggaagtcacccgtact 1801  
QY 241 cccaaatctccaaagcctatcaagtttgagcttctggtgcaccagcatgaagacatac 300  
|||||  
Db 1802 cccaaatctccaaagcctatcaagtttgagcttctggtgcaccagcatgaagacatac 1861  
QY 301 cgagctaaattctgtgagttatgtaccgacggccgagctgtgcacccccccacagaaaccacc 360  
|||||  
Db 1862 cgagctaaattctgtgagttatgtaccgacggccgagctgtgcacccccccacagaaaccacc 1921  
QY 361 acctgcgggtgagttcaagtcccttgacggcgaggttcattgaagaagaacatgatgttc 420  
|||||  
Db 1922 acctgcgggtgagttcaagtcccttgacggcgaggttcattgaagaagaacatgatgttc 1981  
QY 421 atcaagacctgtgctgcattcaactgcccggagagacatacacatctttgaaatcgctg 480  
|||||  
Db 1982 atcaagacctgtgctgcattcaactgcccggagagacatacacatctttgaaatcgctg 2041  
QY 481 tactacaggaagatgtacggagacatggca 510  
|||||  
Db 2042 tactacaggaagatgtacggagacatggca 2071

## RESULT 10

US-09-054-274-1 ; Sequence 1, Application US/09054274  
; Patent No. 6150101  
; GENERAL INFORMATION:  
; APPLICANT: University of South Florida  
; APPLICANT: Grotendorst, Gary R.  
; APPLICANT: Bradham, Jr., Douglas M.  
; TITLE OF INVENTION: METHODS OF IDENTIFYING A COMPOSITION  
; TITLE OF INVENTION: THAT ALTERS CONNECTIVE TISSUE GROWTH  
; TITLE OF INVENTION: FACTOR EXPRESSION (Amended)  
; FILE REFERENCE: 07414/003004  
; CURRENT APPLICATION NUMBER: US/09/054,274  
; EARLIER FILING DATE: 1998-04-02  
; EARLIER APPLICATION NUMBER: 08/386,680  
; EARLIER FILING DATE: 1995-02-10  
; EARLIER APPLICATION NUMBER: 08/459,717  
; EARLIER FILING DATE: 1995-06-02  
; EARLIER APPLICATION NUMBER: 08/167,628  
; EARLIER FILING DATE: 1993-12-14  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2970  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1025)...(2074)  
US-09-054-274-1

Query Match 100.0%; Score 510; DB 3; Length 2998;  
Best Local Similarity 100.0%; Pred. No. 1.le-138;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcttaccgactggaagacacgtttggcccagaccacaaactatgattagagccaactgc 60  
|||||  
Db 1562 gcggcttaccgactggaagacacgtttggcccagaccacaaactatgattagagccaactgc 1621  
QY 61 ctggttcagaccacagagtgagcgctgttccaagacctgtgtggatgggcatctccacc 120  
|||||  
Db 1622 ctggttcagaccacagagtgagcgctgttccaagacctgtgtggatgggcatctccacc 1681  
QY 121 cgggtttaccaatgacacgcctcctcaggctgagagaagcagagccgcctgtgcatggctc 180  
|||||  
Db 1682 cgggtttaccaatgacacgcctcctcaggctgagagaagcagagccgcctgtgcatggctc 1741

QY 181 agccttggaagctgacctgggaaggaacattaaagaaggcgaaggaagtcacccgtact 240  
|||||  
Db 1742 agccttggaagctgacctgggaaggaacattaaagaaggcgaaggaagtcacccgtact 1801  
QY 241 cccaaatctccaaagcctatcaagtttgagcttctggtgcaccagcatgaagacatac 300  
|||||  
Db 1802 cccaaatctccaaagcctatcaagtttgagcttctggtgcaccagcatgaagacatac 1861  
QY 301 cgagctaaattctgtgagttatgtaccgacggccgagctgtgcacccccccacagaaaccacc 360  
|||||  
Db 1862 cgagctaaattctgtgagttatgtaccgacggccgagctgtgcacccccccacagaaaccacc 1921  
QY 361 acctgcgggtgagttcaagtcccttgacggcgaggttcattgaagaagaacatgatgttc 420  
|||||  
Db 1922 acctgcgggtgagttcaagtcccttgacggcgaggttcattgaagaagaacatgatgttc 1981  
QY 421 atcaagacctgtgctgcattcaactgcccggagagacatacacatctttgaaatcgctg 480  
|||||  
Db 1982 atcaagacctgtgctgcattcaactgcccggagagacatacacatctttgaaatcgctg 2041  
QY 481 tactacaggaagatgtacggagacatggca 510  
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Db 2042 tactacaggaagatgtacggagacatggca 2071

## RESULT 11

US-09-056-704-1 ; Sequence 1, Application US/09056704  
; Patent No. 6232064  
; GENERAL INFORMATION:  
; APPLICANT: University of South Florida  
; APPLICANT: Grotendorst, Gary R.  
; APPLICANT: Bradham, Jr., Douglas M.  
; TITLE OF INVENTION: METHODS OF DIAGNOSING A PATHOLOGY  
; TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE  
; TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE  
; TITLE OF INVENTION: TISSUE GROWTH FACTOR (Amended)  
; FILE REFERENCE: 07414/003002  
; CURRENT APPLICATION NUMBER: US/09/056,704  
; EARLIER FILING DATE: 1998-03-03  
; EARLIER APPLICATION NUMBER: 08/386,680  
; EARLIER FILING DATE: 1995-02-10  
; EARLIER APPLICATION NUMBER: 08/459,717  
; EARLIER FILING DATE: 1995-06-02  
; EARLIER APPLICATION NUMBER: 08/167,628  
; EARLIER FILING DATE: 1993-12-14  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2970  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1025)...(2074)  
US-09-056-704-1

Query Match 100.0%; Score 510; DB 4; Length 2998;  
Best Local Similarity 100.0%; Pred. No. 1.le-138;  
Matches 510; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcttaccgactggaagacacgtttggcccagaccacaaactatgattagagccaactgc 60  
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Db 1562 gcggcttaccgactggaagacacgtttggcccagaccacaaactatgattagagccaactgc 1621  
QY 61 ctggttcagaccacagagtgagcgctgttccaagacctgtgtggatgggcatctccacc 120  
|||||  
Db 1622 ctggttcagaccacagagtgagcgctgttccaagacctgtgtggatgggcatctccacc 1681  
QY 121 cgggtttaccaatgacacgcctcctcaggctgagagaagcagagccgcctgtgcatggctc 180  
|||||



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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1158 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-844-188-45

Query Match          7.1%; Score 36; DB 3; Length 1158;
Best Local Similarity 48.1%; Pred. No. 0.21;
Matches 102; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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DB 945 CACCTCCCTCGAGCTGTACCGCTACACGCGCAGGATCAAGATCATGGACATCGAGAC 1004
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QY 114 ctccaccgggttaccaatgacaacgctcctcagcagctagagaagcagcgccctgtg 173
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 174 catggtcagcgcttggaagctgacccctggaagacattaaagaggcgaagagtgcat 233
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1065 GCTGACCAACCACTCTACAGAGGTGGAGGATCACCAGATCCCGAAGCACACCT 1124
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QY 234 ccgtactcccaaatctcccaagctatcaagt 265
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DB 1125 CATCAAGCTCAAGAAGCACTACTTCAAGAAGT 1156
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RESULT 14
US-08-866-340-13/c
; Sequence 13, Application US/08866340
; Patent No. 6020318
; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
; TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: United States of America
; ZIP: 02109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,340
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Keown, Wayne A.
; REGISTRATION NUMBER: 33,923
; REFERENCE/DOCKET NUMBER: 106.101.187
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-866-340-13
Query Match          6.7%; Score 34.2; DB 3; Length 293;
Best Local Similarity 60.0%; Pred. No. 0.42;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 123 ggttaccaatgacaacgcctcctcagcagctagagaagcagcgccctgtgcatggtcag 182
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DB 249 GGTTCACAGTCACATGGCCTTCTGCAAGCCTGTGAGAAATTCACCACGAGAGCCCGTCAG 190
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QY 183 gccttgcaagctgacctggaagagaacattaaga 217
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RESULT 15
US-09-103-875-17/c
; Sequence 17, Application US/09103875A
; Patent No. 6221849
; GENERAL INFORMATION:
; APPLICANT: Szyf, Moshe
; APPLICANT: Bigey, Pascal
; APPLICANT: Ramchandani, Shyam
; TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDES
; FILE REFERENCE: 106101.194
; CURRENT APPLICATION NUMBER: US/09/103,875A
; CURRENT FILING DATE: 1998-06-24
; EARLIER APPLICATION NUMBER: 60/069,865
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 08/866,340
; EARLIER FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-103-875-17

Query Match          6.7%; Score 34.2; DB 4; Length 293;
Best Local Similarity 60.0%; Pred. No. 0.42;
Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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DB 249 GGTTCACAGTCACATGGCCTTCTGCAAGCCTGTGAGAAATTCACCACGAGAGCCCGTCAG 190
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QY 183 gccttgcaagctgacctggaagagaacattaaga 217
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DB 189 CCCCCAGGAGGAGAACATGAAGGCCCTTTTCAGA 155
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Search completed: August 20, 2001, 22:08:26
Job time: 2527 sec
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us-09-461-646-1\_copy\_667\_1176.rni

Tue Aug 21 08:16:52 2001

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 20, 2001, 21:23:54 ; Search time 1173.23 Seconds  
(without alignments)  
4109.131 Million cell updates/sec

Title: US-09-461-646-l\_COPY\_667\_1176  
Perfect score: 510  
Sequence: 1 gcggctaccgactggaaga.....agatgtacggagacatggca 510

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Thu Aug 21 08:16:53 2001

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



us-09-461-646-1-copy\_667\_1176.rst

Tue Aug 21 08:16:53 2001

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SOURCE
ORGANISM      human.
LOCUS         Homo sapiens
DEFINITION    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 854)
AUTHORS       Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
               Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
               Isogai, T.
TITLE         HRI human cDNA project
COMMENT       Unpublished (2000)
               Contact: Takao Isogai
               Genomics Laboratory
               Helix Research Institute
               1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
               Tel: 81-438-52-3951
               Fax: 81-438-52-3952
               Email: genomics@hri.co.jp
               HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
               Research Institute; cDNA library construction: Department of
               Virology, Institute of Medical Science, University of Tokyo, and
               Helix Research Institute.
FEATURES     Location/Qualifiers
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Best Local Similarity 97.1%; Pred. No. 9.2e-125;
Matches 470; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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DB 360 CTGTGTCAGACACACAGAGTGAGCGGCTGTTCACAGACCTGTGGATGGCATCTCCACC 419
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DB 660 ACCTTGCCTGGTGGAGTTCAAGTGCCTGACGCGGANGTGCATGAAGAAGAAGATGATTC 719
QY 421 atcaagacctgtgctgocattacaactgtcccgagacacatgacatctttgaatcgtg 480
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QY 481 tact 484
DB 780 TACT 783

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ACCESSION     BG116765
VERSION       BG116765.1 GI:12610352
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 963)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
               Email: cgabbs@mail.nih.gov
               Tissue Procurement: ATCC
               cDNA Library Preparation: Life Technologies, Inc.
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
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               Technologies. Note: this is a NIH_MGC Library."
BASE COUNT    236 a 244 c 262 g 221 t
ORIGIN
Query Match   88.8%; Score 453; DB 174; Length 963;
Best Local Similarity 99.8%; Pred. No. 4.7e-122;
Matches 464; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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DB 61 ATGGGCATCTCCACCGGGTTACCAATGACACGCCCTCTCTGCGAGGTAGAGAAGCAGAGC 120
QY 166 cgcctgtgcatggtcaggccttgcgaagctgacctggaagagaacattaaagaaggcaaa 225
DB 121 GCCTGTGCTATGGTTCAGGCCCTTGCGAAGCTGACCTGGAGAGAACATTAAGAAGGCCAAA 180
QY 226 aagtgcactccctactcccaaaatctccaaagcctatcaagtttgcgcttctgctgcacc 285
DB 181 AAGTGCATCCGTACTCCCAAAATCTCCAAAGCTATCAAGTTTGAGCTTTCTGCTGCACC 240
QY 286 acatgaagacataccagagctaaattctgtggagtgtatgtaccgagccgctatgtcacc 345
DB 241 AGCATGAAGACATACCGAGCTAAATCTGTGGAGTATGTACCGACGCGCATGTGTCACC 300
QY 346 cccacagaaacacacccctgcggtgagttcaagttccctgacgagcgaggtcatgaag 405
DB 301 CCCCACAGAACCAACCAACCCCTGCCGGTGGAGTTCAAGTCCCTGACGCGGAGGTCAATGAAG 360

```

```

QY 406 aagaacatgttctatcaagaacctgtgcctgcattacacactgtcccgagagacaatgac 465
|||||
Db 361 AAGAACATGATGTTTCATCAAGACGTGTGCTGCCTGCATTACAACCTGCTCCGGAGACAATGAC 420
|||||
QY 466 atcttgaatcgtgtactacagaagatgtacgagacatggca 510
|||||
Db 421 ATCTTTGAATCGCTGTACTACAGAAGATGTACGGAGACATGGCA 465
|||||

RESULT 4
LOCUS AW742404 678 bp mRNA EST 07-SEP-2000
DEFINITION up56f10.y1 Soares_mouse_NMIE Mus musculus cDNA clone IMAGE:2780107
5' similar to gb:M80263 Mouse mRNA sequence (MOUSE):..
ACCESSION AW742404
VERSION AW742404.1 GI:7654192
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 678)
AUTHORS NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco
High quality sequence stop: 471.
FEATURES
source
1..678
Location/Qualifiers
/organism="Mus musculus"
/strain="C3H x 101 (F1 stock)"
/db_xref="taxon:10090"
/clone="IMAGE:2780107"
/clone_lib="Soares_mouse_NMIE"
/sex="male"
/dev_stage="newborn"
/lab_host="DH108"
/notes="Organ: Inner ear, 170 pooled; Vector: pT73D-Pac;
Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed
with a Not I - oligo(dT) primer [5,
TGTTCACATCAGTGAAGTGGAGCGGCGGACACTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
is normalized, and was constructed and donated by Bento
Soares and M.Fatima Ronaldo (University of Iowa) and R.
Hardisty, A. Varela-Carver, P. Mburu and S.D.M. Brown (MRC
UK Mouse Genome Centre and Mammalian Genetics Unit,
Harwell, UK)."
BASE COUNT 187 a 173 c 172 g 146 t
ORIGIN

Query Match 84.7%; Score 432.2; DB 120; Length 678;
Best Local Similarity 90.6%; Pred. No. 5.4e-116;
Matches 461; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 gcgcttaccgactgaagacgtttggccgaccccaactatgattagcaactgc 60
|||||
Db 57 GCGCTTACCGACTGGAAGACATTTGGCCACACCCCAACTATGATGAGCGCAACTGC 116
|||||
QY 61 ctggtccagaccacagagtggcgctgttccaagacctgtggatggcgatctccacc 120
|||||
Db 117 CTGGTCAGACCACAGATGGCGCTGTCTTAAGACCTGTGGAATGGGCATCTCCACC 176
|||||
QY 121 cgggttaccatgacacgcctctcctcaggtctagagaagcagacgcctgtgcatggtc 180
|||||

```

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Db 177 CGAGTTACCAATGACAATACCTTCTGCAGACTGGAGAAGCAGAGCCCGCTCTGCATGGTC 236
QY 181 aggccttcgaagctgacctgggaagaaacattaaagaagggaacaaagtgcacccgtact 240
|||||
Db 237 AGGCCCTGCGNAGCTGACCTGGAGGAAAACATTAAAGAGGGCAAAAGTGCATCCGGACA 296
|||||
QY 241 cccaaaatctccaaagcctatcaagtgttgagcttctgtgcaccagcatgaagacatac 300
|||||
Db 297 CCTAAAATCGCCAAAGCCTGTCAAGTTTGAGCTTTCTGCTGCACCCAGTGTGAAGACATAC 356
|||||
QY 301 cgagctaaattctgtggagtgtaccgacggccgcatgtgcacccccacacagaaccacc 360
|||||
Db 357 AGGCTTAAGTTCTCGGGGTGTGCACAGAGCGGCGCTGCTGCACACCGCACAGAACCAACC 416
|||||
QY 361 accctgcggtggagttccaagtgccttgaaggcgaggtcattcatgaagaagaacatatttc 420
|||||
Db 417 ACTCTGCCAGTGGAGTTCAATGCCCGATGGCGAGATCATGAAAAGAAATATGATGTC 476
|||||
QY 421 atcaagacctgtgcctgccattacaactgtcccgagagacaatgacatctttgaatcgctg 480
|||||
Db 477 ATCAAGACCTGTGCTGCCATTACAACCTGTCTGGGACAATGACATCTTTGAGTCCTCGT 536
|||||
QY 481 tactacaggaagatgtacggagacatggc 509
|||||
Db 537 TACTACAGGAAGATGTACCGAGACATGGC 565
|||||

RESULT 5
AA187390
LOCUS AA187390 487 bp mRNA EST 10-MAR-1998
DEFINITION zp70a06.r1 stratagene endothelial cell 937223 Homo sapiens cDNA
clone IMAGE:625522 5' similar to gb:M92934 CONNECTIVE TISSUE GROWTH
FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AA187390
VERSION AA187390.1 GI:1773616
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 862 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 340.
Location/Qualifiers
1..487
/organism="Homo sapiens"
/db_xref="GDB:5047676"
/db_xref="taxon:9606"
/clone="IMAGE:625522"
/clone_lib="Stratagene endothelial cell 937223"
/dev_stage="umbilical vein, 1 passage"
/lab_host="SOLR (kanamycin resistant)"
/notes="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Umbilical vein endothelial cells, passaged once. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

```

RESULT	7			
AA221075	96 bp	mRNA	EST	12-FEB-1997
LOCUS	MW5C04.r1	Soares mouse	3NWE12.5	Mus musculus cDNA clone
DEFINITION	inframe:660870 5' similar to gb:M70641 Mouse FISP-12 protein (MOUSE )	: mRNA sequence.		
ACCESSION	AA221075			
VERSION	AA221075.1	GI:1840244		
KEYWORDS	house mouse.			
SOURCE	Mus musculus			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognatha; Muridae; Murinae; Mus			
REFERENCE	1 (bases 1 to 696)			
AUTHORS	Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.			
TITLE	The WashU-HHMI Mouse EST Project			
JOURNAL	Unpublished (1996)			
COMMENT	Contact: Maria M/Mouse EST Project washu-hhmi Mouse EST Project			

BASE COUNT	133 a	134 c	121 g	95 t	4 others
Query Match	80.5%	Score 410.4	DB 3	Length 487	
Best Local Similarity	97.7%	Pred. No. 1.2e-109			
Matches 477	Conservative	0	Mismatches 5	Indels 6	Gaps 6
QY	20	acacgtttggccagacccaactatgattagagccaactgctctggtccagacacagagt	79		
DB	1	ACACGTTTGGCCACACCCNACTATGATTAGAGCAACTGCTGCTGGTCCAGACCACAGAGT	60		
QY	80	ggagcgccctgtttccaaagaccttggaatggggcatctccaccgggttaccgaatgacaacy	139		
DB	61	GANGCGCCCTGTTCCAAAGACCTGTGGGATGGGGATCTCCACCGGGTTACCAATGACAACG	120		
QY	140	ctctctcaggcttagaagacagagccgccc-tgtgcatgggtcaggcccttgagagcgtgac	198		
DB	121	CCCTCTCGAGCTTAGAGAGCAGCAGNCNGCCGTGTCATGGTCAGGCTTGGCAA-NTGAC	179		
QY	199	ctggaagagaacattaagaaggggcaaaagtgcctccttaactcccaaatctccaagcct	258		
DB	180	CTGGAAGAGAACAATTAAGAGGGCAAAAAGTGCATCCGTACTCCCAAAATCTCCAAGCCT	239		
QY	259	atcaagtttagctttctagctcacccagcatgaagacataccagagctaaaattctgtgga	318		
DB	240	ATCAAGTTTGAGCTTCTGGCTGCACCATGACATGACATACCGAGCTAAATTCGTGTGA	299		
QY	319	gtatgtaccgacgg-ccgatgtgtccccccccccagacacacacccctgcggtgg-agt	376		
DB	300	GTATGTACCGAGCGCCGATGCTGCACCCCCCAGAACACACCCCTGCCGTGGAAGT	359		
QY	377	tcagtgcccttgagcggg-aggtcataagaagaacatgatgttcacgaacctgtgccc	435		
DB	360	TCAAAGTGCCTTGACGGGGAGGTCATGAAGAGACATGATGTTTCATCAAGACCTGTGOC	419		
QY	436	tgcattacaac-tgtcccgagacaatgatcatcttgaatcgtctgtactacagaagat	494		
DB	420	TGCCATTACACTTGTCCCGGAGACAATGACATCTTTGAATCGCTGTACTACAGGAAGAT	479		
QY	495	gtacggag 502			
DB	480	GTACGGAG 487			
RESULT	6				
AL547439	879 bp	mrna	EST	16-FEB-2001	
LOCUS	AL547439	LTI_NFL006_PL2	Homo sapiens	cDNA clone	CS0DI011YE17 5
DEFINITION	prime, mrna	sequence.			
ACCESSION	AL547439				
VERSION	AL547439.1	GI:12881511			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 879)				
JOURNAL	Li, W. B., Gruber, C., Jessee, J. and Polayes, D.				
COMMENT	Full-length cDNA libraries and normalization				
	Unpublished (2001)				
	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				
	BP 191 91006 EVRY cedex - France				
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.				
FEATURES	Location/Qualifiers				
source	1..879				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="CS0DI011YE17"				
	/clone_lib="LTI_NFL006_PL2"				
	/tissue_type="placenta"				
	/note="vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA"				

Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:406718

Seq primer: -28ml3 rev2 ET from Amersham  
 High quality sequence stop: 499.

# FEATURES

source  
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 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:660870"  
 /clone\_lib="Soares mouse 3NME12 5"  
 /sex="unknown"  
 /tissue\_type="fetus"  
 /dev\_stage="12.5dpc total fetus"  
 /lab\_host="DH10B"  
 /notes="Organ: whole fetus; Vector: pT7T3D-Pac (Pharmacia)  
 with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Not I - oligo(dT) primer.  
 [5' TGTTACCAATCTGAAGTGGAGCGCGCTTATTTTTTTTTTTTTTTT  
 3'], on total mouse RNA [provided by Minoru Ko, Wayne  
 State Univ.]; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pT7T3 vector.  
 Library went through one round of normalization, and was  
 constructed by Hento Soares and M. Fatima Bonaldo."  
 200 a 174 c 169 g 152 t 1 others

BASE COUNT  
 ORIGIN

Query Match 80.3%; Score 409.4; DB 4; Length 696;  
 Best Local Similarity 90.5%; Pred. No. 2.6e-109;  
 Matches 448; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 15 ggaagacacgtttggccagaccacattatgattagagccaactgctgtccagaccac 74  
 DB 15 GGAAGACACATTTGGCCAGACCCCACTATGATGCGAGCCCACTGCTGTCCAGACAC 74  
 QY 75 agagtggagcgcctgttccaaagacctgtggatgggcatctccaccgggttaccatga 134  
 DB 75 AGACT-GAGCGCCTGTTCTAAGACCTGTGGATGGGCATCTCCACCGAGTTACCAATGA 133  
 QY 135 caacgcctctgaggttagaagaagagagccgcctgtgcatgtcagggccttcgaagc 194  
 DB 134 CAATACCTTTGACAGCTGGAGAAAGCAGACCGCGCTCTGCATGTGTCAGGCCCTCGAAGC 193  
 QY 195 tgacctggaagagacatttaagaaggagcaaaagtgcctcgtactcccaaatctccaa 254  
 DB 194 TGACCTGGAGAAACATTAAGAAGGCAAAAAGTGTATCGGACACCTAAATTCGCCAA 253  
 QY 255 gctatcaagtgttagctttctggtcgcaccagcatgaagacataccagagctaaattctg 314  
 DB 254 GCCTGTCAAGTTTCAAGCTTTCTGCTGTCACCCAGGTGTAAGACATACAGGGCTAAGTCTG 313  
 QY 315 tggagtattaccgagcggcgatgctgcacccccccacagacacccacctgcccgtgga 374  
 DB 314 CGGGGTGTGCACAGACGCGCGCTGCTGCACACCGCAGACAGAACCCACTCTGCGCAGTGA 373  
 QY 375 gttaagtgcctgacggcggaggtcatgaagaagaacattgttctcatcaagacctgtgc 434  
 DB 374 GTTCAATGCCCCGATGCGGAGATCATGAAGAAGAAATATGATGTTATCAAGACCTGTGC 433  
 QY 435 ctgccattacaactgtcccgagagacaatgcattcttgaatcgctgtactacaggaagat 494  
 DB 434 CTGCCATTACAACGTCTCTGGGACAAATGACATCTTTGAGTCCCTGTACTACAGGAAGAT 493  
 QY 495 gtacggagacatggc 509  
 |||||||

Db 494 GTACGGAGACATGCG 508

## RESULT

8  
 AA373233

LOCUS

DEFINITION

AA373233

ACCSSION

AA373233.1

VERSION

AA373233.1

KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 436)

AUTHORS

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult

,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White

,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,

Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald

,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,

Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,

Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.

,Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kosak,D.L.,

Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,

Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon

,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and

Venter,J.C.

TITLE

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL

MEDLINE

COMMENT

Other\_ESTS: THC166347

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..436

/organism="Homo sapiens"

/db\_xref="ATCC (Inhost):177595"

/db\_xref="taxon:9606"

/clone\_lib="HSCI72 cells 1"

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/cell\_line="HSCI72 (16PDL)"

/dev\_stage="fetal"

/note="Organ: lung; Vector: pBluescript SK-; Site\_1: EcoRI

; Site\_2: XhoI"

BASE COUNT 115 a 122 c 115 g 82 t 2 others

ORIGIN

Query Match 78.8%; Score 402; DB 6; Length 436;

Best Local Similarity 97.9%; Pred. No. 3.4e-107;

Matches 427; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 1 gcgcctaccagactggagacacgtttggccagaccacattatgattagagccaactgc 60

DB 2 CGCGCTTACCGACTGGAGACACGTTTGGCCCCAGACCACTATGATGATAGACCACTGC 61

QY 61 ctggtccagaccagagtgagcgctgttccaaagacctgtggatgggcatctccacc 120

was primed with a Not I - oligo(Gr) primer [5',  
TGTTCACCAATCTGAAGTGGGCGCGCGAGTTTTTTTTTTT 3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(M. Fatima Bonaldo, library constructed by Bento Soares and  
M. Fatima Bonaldo, RNA from normal foreskin melanocytes  
(FS374) was kindly provided by Dr. Anthony P. Albino.  
143 °C 133 g 128 t 4 others

BASE COUNT	169 a	143 c	133 g	128 t	4 others
ORIGIN					

Query Match	77.3%	Score 394;	DB 159;	Length 577;
Best Local Similarity	99.3%	Pred. No. 8.3e-105;		
Matches 416: Conservative	0;	Mismatches 1;	Indels 2;	Gaps 2;

92	QY	ccaagaactgtggatggcgtatccaccgcgggttaccacatgacaacgcctctcgcaggc	151
1	DB	ccaagacctgtgggatgggcattccaccgcgggttaccacatgacaacgcctctcgcaggc	60
152	QY	tagaagaacagagccgcctgtgcatggtcagggccttgcgaagctgacctggagaagaaca	211
61	DB	tagaagaacagagccgcctgtgcatggtcagggccttgcgaagctgacctggagaagaaca	118
212	QY	ttaagaaggcacaagaatgcatcgctactcccaaaatctccaagcctatacaagttggagc	271
119	DB	tttaagaaggcacaagaatgcatcgctactcccaaaatctccaagcctatacaagttggagc	178
272	QY	ttttcggctgcaccagcatgaagacataccgagctaaattctgtggagtatgtaccgcagc	331
179	DB	ttttcggctgcaccagcatgaagacataccgagctaaattctgtggagtatgtaccgcagc	238
332	QY	gcgcgatgtgcacccccccacagaaacaccacccctgccggtggagttcgaagtcgccctgacg	391
239	DB	gccgatgtcgtcacccccccacagaaacaccacccctgccggtggagttcgaagtcgccctgacg	298
392	QY	gcgcgatcatgaagaagaacatgatttcatacaagacctgtgcctgcattacaactgtc	451
299	DB	gcgcgggttcatagaagaacatgatgttcatacaagacctgtgcctgcattacaactgtc	358
452	QY	ccgcgaacaatgacatcttttgatcgcgtgtactacagaagaatgtacgcgagacatggca	510
359	DB	ccgcgaacaatgacatcttttgatcgcgtgtactacagaagaatgtacgcgagacatggca	417

RESULT	10	EST	21-SEP-2000
BE816120	595 bp	mRNA	
LOCUS			CDNA, mRNA sequence

VERSION BE816120.1 GI:10248354  
EST.  
KEYWORDS human.  
SOURCE

ORGANISM	REFERENCE
Homo sapiens	1 (bases 1 to 595)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

**REFERENCE**

1<sup>\*</sup> (bases 1 to 595)

NAGAI, M., E. GARCIA CORREA, R., VERJOVSKI-ALMEIDA, S., BRIONES, M.R., NEGAS, N.E.A., da SILVA, W. Jr., ZAGO, M.A., BORDIN, S., COSTA, F.F., NEGRU, M.A., BALA, G.S., MATSUMURA, A., BAIA, G.S., SIMPSON, D.H., GOLDMAN, G.H., CARVALHO, A.F., CARVALHO, P., JONGENEEL, C.V., O'HARE BRUNSTEIN, A., deOLIVEIRA, S., BUCHER, P., de SOUZA, S.J., and M.J., SOARES, F., BRENTANI, I.R.R., REIS, L.F., and Simpson, A.J.J. expressed

TITLE
Shotgun sequencing of the human transcriptome with one expressed sequence tag per gene
U S A   97 (7) : 3491-3496 (2000)

JOURNAL  
MEDLINE  
Proc. Natl. Acad. Sci. U.S.A. 97 (1998) 1512-1516  
20202663  
Contact: Simpson A.J.G.

CONTACT: SARA L. GONCALVES  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922

62	CTGGTCAGACACAGAGTGNAGGCCTGTTC	AAAGACCTGTGGGATGGGCATCTCCACC	121	
121	CGGGttaccaaatgaacagcctctcgaggta	gagaagcagagccgcctgtgcattgctc	180	
122	CGGGTTTACC	AAATGACAACGCCCTCTCGAGGCTAGAGA	AGCAGAGCCGCTGTGTGCATGTGC	181
181	aggccttgcgaagctgacctggagaagaa	cattaaagaaggcaaaaagtgcctcgctact	240	
182	AGGCCTTTGCGAAATGGACCTGGAAGAGA	AACATTTAGAAAGGGCAAAAGTGCATTCGTACT	241	
241	cccaaaatctccaaagcctatccaaagttd	gagctttctgtgctgcaccagcatgaagacatac	300	
242	CCCAAAATCTCCAAAGCCTATCAAGTTTG	AGCTTTCTGCTGTCACACGATGAGACATAC	301	
301	cgagctaaattctgtggagtatgtaccga	cggccgagatctgcaccccccacagaacccac	360	
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ACCESSION N32344  
VERSION N32344.1 GI:1152743  
KEYWORDS EST.

SOURCE: human.  
ORGANISM: Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eumammalia; Placentalia; Eutheria; Hominid; Hominidae; Homininae; Hominini; Homo.

REFERENCE  
1 (bases 1 to 577)  
Mammalia: Eutheria; Primates; Catarrhini; Hominoidea.  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Ho-  
llister, L., Leamon, G., Marrara, M., Parsons,  
R., Hultman, M., Kucaba, T., Le, M., Leonon, G., Marrara, M., Parson,  
M., Hultman, M., Tan, F., Trevaskis, E., Water-  
Riffin, L., Rohlfing, T., Soares, M., Tardiff, R., Reichmann, P. and Wilson, R.

R., WILLIAMSON, A.; WOLFGANG, E. THE WASHN-MERCK EST PROJECT

TITLE  
 JOURNAL  
 COMMENT  
 Unpublished (1995)  
 Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
314 285 1900

Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)

High quality sequence stops: 340  
Source: IMAGE Consortium, LLNL  
available royalty-free through LLNL ; contact t

Insert Length: 1770 Std Error: 0.00  
IMAGE Consortium (info@image.llnl.gov) for further information  
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polylinker; Site_1: Not I; Site_2: Eco RI; 1st stra

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Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC5-BN0193-140  
600-032-BN018t3-2000-06-14&t4=1)  
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High quality sequence stop: 357.

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/dev\_stage="Adult"  
/note="Organ: breast\_normal; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
177 a 147 c 135 g 136 t

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QY 135 caacgctctgcaggctagagagcagccgctgtgcattgctcagcgttcgcgaagc 194  
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Db 63 TGACCTGGAAGAAACATTTAAGAGGGCAGAAAGTGCCTACTCCCAAAATCTCCAA 122  
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Db 123 GCCTATCAAGTTTGAGCTTTCTGGCTGCACCATGATGAGCATACCGAGCTAAATCTG 182  
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VERSION BE166172.1 GI:8628893  
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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 415)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

TITLE

JOURNAL  
MEDLINE  
COMMENT

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-MR3-HT0489-250  
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High quality sequence stop: 415.

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Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
76 a 109 c 126 g 104 t

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Db 366 CGGCTTACCAGCTGGAAGACACGTTTGGCCACAGCCCACTATGATTAGAGCCCACTGC 307  
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Db 306 CTGGTCCAGACCACAGAGTGGAGCGCCTGTTCAGACCTGTGGATGGGCATCTCCACC 247  
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Db 246 CGGTTTACCATGACAACGCGCTCTCTCAGGCTAGAGAAGCAGCGCCCTGCGCATGTC 187  
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QY 361 accc 364  
Db 6 CACC 3  
RESULT 12

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VERSION	BF082233.1	GI:10876063	
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AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL ( <a href="http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-MR0-BN0115-210">http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-MR0-BN0115-210</a> ) 800-006-g03et3-2000-08-21et4-1 Seq primer: puc 18 forward High quality sequence start: 44 High quality sequence stop: 631 Location/Qualifiers		
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Db	162	GCTTTCTGGCTGCGACAGCATGAGACATACCGAGCTAAATTTCTGTGGAGTATGACCGA	221
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Qy 254 agcctataagtttgagcttcttgctgacccagcatgaagacataccgagctaaattct 313
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Qy 314 gtgagtgatgtaccgagcgccgatgtgctgaccccccacagaaacacacccctgcctg 373
Db 204 GTGAGTATGTACCGACGCGCGATGCTGCGACCCCGACACACCCACCTGCGCGTGG 263
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VERSION BE479129.1 GI:9598662
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SOURCE Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 388)
AUTHORS Sonstegard,T.S., Capuco,A.V., Van Tassel,C.P., Ashwell,M.S. and
Wells,K.D.
TITLE Mapping of Expressed Sequence Tags from a normalized bovine mammary
gland cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tadselpsi@barc.usda.gov
Single pass sequencing. Bases called and alt.trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
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FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCCAGCAGC
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ORIGIN
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Db 181 TTCTGCGGAGTGTGCACAGCGGGCGTGTGACCCCGGAGACAATGATCTTCGAGTCACGTACTACAGG 240
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Db 301 TGTGCTGCCATTACAACCTGCCCGGAGACAATGATGATCTTCGAGTCACGTACTACAGG 360
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Db 361 AAGATGTATGAGACATGGC 380

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VERSION BF162951.1 GI:11043187
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SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 800)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaphs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9183 row: a column: 14
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
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Tue Aug 21 08:16:53 2001

Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH

BASE COUNT  
ORIGIN

187 a 219 c 233 g 161 t

Query Match 66.5%; Score 339.4; DB 145; Length 800;  
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QY 181 aggccttcgaaagctgacctgagagagacattaaagaa-gggcaaaagtgcacccgtac 239  
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Job time: 1349 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2001, 22:04:44 ; Search time 61.48 Seconds  
(without alignments)  
167.633 Million cell updates/sec

Title: US-09-461-646-2\_COPY\_180\_349

Perfect score: 948

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 21: /SIDS1/gcgdata/geneseq/geneseq/AA2000.DAT:\*
- 22: /SIDS1/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	172	21	AAV92941
2	948	100.0	347	18	AAW12694
3	948	100.0	349	16	AAW79964
4	948	100.0	349	18	AAW09089
5	948	100.0	349	19	AAW11302
6	948	100.0	349	18	AAW62084
7	948	100.0	349	20	AAW18361
8	948	100.0	349	20	AAW81425
9	948	100.0	349	21	AAV92939
10	948	100.0	349	21	AAV92940
11	948	100.0	349	21	AAV44755

#### ALIGNMENTS

RESULT 1

AAV92941  
ID AAV92941 standard; Protein; 172 AA.

XX AC AAV92941;

XX DT 08-NOV-2000 (first entry)

XX DE Human connective tissue growth factor protein fragment.

XX KW Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;  
KW fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;  
KW hypertrophic scarring; atherosclerosis; diabetic nephropathy; retinopathy;  
KW hypertension; cardiovascular disorder; wound healing; bone repair.

XX OS Homo sapiens.

XX PN WO200035939-A2.

XX PD 22-JUN-2000.

XX PF 14-DEC-1999; 99WO-US29654.

XX PR 14-DEC-1998; 98US-0112240.

XX PR 14-DEC-1998; 98US-0112241.

XX PA (UYMI-) UNIV MIAMI.

XX PA (FIBR-) FIBROGEN INC.

XX PI Grotendorst GR, Neff TB;

XX DR WPI; 2000-431568/37.

XX DR N-PSDB; AAA11281.

XX

Human connective t  
Human connective t  
Rat connective tis  
Beta-IG-M2. Mus m  
Murine Fisp12. Mu  
Mouse connective t  
Amino acid sequenc  
Bovine connective  
Mouse connective t  
Rat connective tis  
Human cancer assoc  
Bovine mammary tis  
Chicken nov protei  
Beta-IG-M1. Mus m  
Human cysteine ric  
Human monocyte mat  
Human cancer assoc  
Connective tissue  
Human CTGF-2. Hom  
Mouse putative mat  
Mouse WISP-1 prote  
Human WISP-3 prote  
Human putative mat  
Human connective t  
Human WISP-3 prote  
Human growth facto  
Human WISP-1 varia  
Human putative mat  
Human WISP-1 varia  
Human WISP-1 varia  
Human WISP-1 varia  
Human WISP-1 prote

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PT New fragment of connective tissue growth factor (CTGF) polypeptide  
 PT having mitogenic activity, useful in wound healing, bone and tissue  
 PT repair -

PS Disclosure: Fig 3; 71pp; English.

XX This sequence represents a fragment of the human connective tissue  
 CC growth factor (CTGF) polypeptide which has mitogenic activity. The  
 CC sequence covers the amino acids encoded by exons 4 and 5 of the full  
 CC length cDNA sequence (AA112694). The protein can be used to raise  
 CC antibodies which specifically bind to CTGF and are used to treat a  
 CC CTGF-associated disease or disorder, e.g. a fibroproliferative  
 CC disease/disorder such as kidney fibrosis, scleroderma, pulmonary  
 CC fibrosis, liver fibrosis, arthritis, hypertrophic scarring,  
 CC atherosclerosis, diabetic nephropathy and retinopathy, hypertension,  
 CC kidney disorders, angiogenesis-related disorders, skin fibrotic  
 CC disorders, and cardiovascular disorders. The protein is also useful in  
 CC wound healing, bone and tissue repair.

XX Sequence 172 AA;

Query Match 100.0%; Score 948; DB 21; Length 172;  
 Best Local Similarity 100.0%; Pred. NO. 4e-86;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDPMTIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRICMV 60  
 DB 3 aayrledtfgpdpmtiranclvqttewsacsktcgmgistrtvndnascrleqsrilmv 62  
 QY 61 RPEADLEENIKGKKCIKIRPKISKPIKFKELSGCTSMKTYRAKFCGCTDGRCTPHRTT 120  
 DB 63 rpeadleenikgkckirtpkiskpikfkelsgctsmktyrakfcgctdgrctphrtt 122  
 QY 121 TLPVEFKCPDGEVMKNNMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170  
 DB 123 tlpvefkcpdgevmmknnmfiktacachyncpgdndifeslyyrkmygdma 172

## RESULT 2

AAW12694

ID AAW12694 standard; Protein; 347 AA.

XX AAW12694;

DT 31-MAY-1997 (first entry)

XX Connective tissue growth factor.

XX Connective tissue growth factor; CTGF; bone; cartilage; vulnary;

XX wound healing; osteoporosis; osteoarthritis; osteochondrytis.

XX Mus sp.

XX WO9638168-A1.

XX 05-DEC-1996.

XX 31-MAY-1996; 96WO-US08210.

XX 31-MAY-1996; 96WO-US08140.

XX (GROT/) GROTEENDORST G R.

XX Grotendorst GR;

XX WPI; 1997-042658/04.

XX N-PSDB; AAT59618.

XX Connective tissue Growth Factor composition - for inducing bone,  
 PT tissue and cartilage formation and wound healing

XX Disclosure: Fig 1C1-3; 60pp; English.

XX Connective tissue growth factor (CTGF) (AAW12694) is a cysteine-rich  
 CC mitogenic protein which is selectively induced in fibroblasts after  
 CC activation with transforming growth factor beta (TGF-beta).  
 CC Recombinant CTGF can be produced in prokaryotic or eukaryotic host  
 CC cells utilising an isolated CTGF gene (AAT59618). Compsns.  
 CC comprising CTGF, pref. in combination with TGF-beta, are used to  
 CC induce bonding formation, e.g. to treat osteoporosis,  
 CC osteoarthritis and osteochondrytis, to induce tissue and cartilage  
 CC formation, and to induce wound healing. It can also be used in  
 CC culture systems e.g. to expand stem cells or chondrocytes prior to  
 CC re-implantation. CTGF is more stable to protease degradation than  
 CC other growth factors used as prior art wound healing agents.

XX Sequence 347 AA;

Query Match 100.0%; Score 948; DB 18; Length 347;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-86;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDPMTIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRICMV 60  
 DB 178 aayrledtfgpdpmtiranclvqttewsacsktcgmgistrtvndnascrleqsrilmv 237  
 QY 61 RPEADLEENIKGKKCIKIRPKISKPIKFKELSGCTSMKTYRAKFCGCTDGRCTPHRTT 120  
 DB 238 rpeadleenikgkckirtpkiskpikfkelsgctsmktyrakfcgctdgrctphrtt 297  
 QY 121 TLPVEFKCPDGEVMKNNMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 170  
 DB 298 tlpvefkcpdgevmmknnmfiktacachyncpgdndifeslyyrkmygdma 347

## RESULT 3

AAW79964

ID AAW79964 standard; Protein; 349 AA.

XX AAW79964;

DT 12-JUN-1996 (first entry)

XX Connective tissue growth factor.

XX Connective tissue growth factor; CTGF; wound healing; vulnary;  
 XX cell proliferation; cancer; fibrosis; atherosclerosis; diagnosis  
 XX therapy; mitogen.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 28 /label= N-glycosylation\_site

XX Modified-site 225 /label= N-glycosylation\_site

XX US5408040-A.

XX 18-APR-1995.

XX 30-AUG-1991; 91US-0752427.

XX 30-AUG-1991; 91US-0752427.

XX 14-DEC-1993; 93US-0167628.

XX (UYSF-) UNIV SOUTH FLORIDA.

XX Bradham DM, Grotendorst GR;

XX WPI; 1995-161147/21.

XX N-PSDB; AAT04226.

XX New connective tissue growth factor - used to develop prods. for  
 PT

PT wound healing and for diagnosis and therapy of cell proliferative disorders.

XX  
XX  
PS  
XX  
XX  
Claim 1; Column 19-20; 12pp; English.

CC Novel human connective tissue growth factor (CTGF) (AAR79964) is related immunologically and biologically to platelet-derived growth factor (PDGF), but is the product of a distinct gene. CTGF is mitogenic and also a chemotactic agent for cells. It is produced by endothelial and fibroblastic cells, and probably acts as a growth factor in wound healing. Recombinant CTGF can be obtained by expression of cDNA clone DB60R32 (A104226) in transformed host cells. It is used to accelerate wound healing, and to raise antibodies useful in detecting disorders associated with overgrowth of cells, such as cancer, fibrotic diseases and atherosclerosis.

XX  
SQ Sequence 349 AA;

Query Match 100.0%; Score 948; DB 16; Length 349;  
Best Local Similarity 100.0%; Pred. No. 9.2e-86;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLETFGDPPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLKQSLCMV 60  
DB 180 aayrledtfgdpptmirancvlqttewsacsktcgmgistrvtndnascrlkqslcmv 239  
QY 61 RPEADLEENIKGKCIPTPKISKPIKFKELSGCTSMKTYRAKFCGVTGRCCTPHRTT 120  
DB 240 rpeadleenikgkciptpkiskpikfkfslsgctsmktyrakfcgvtgrcctphrtt 299  
QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 170  
DB 300 tlpvefkcpdgevmknmmfiktachyncpgdndifeslyyrkmygdma 349

#### RESULT 4

AAW09089  
ID AAW09089 standard; Protein; 349 AA.

AC AAW09089;

XX  
XX  
DT 26-APR-1997 (first entry)

XX Human connective tissue growth factor.

DE  
DE  
KW Connective tissue growth factor; CTGF; mitogen; cell proliferation;  
KW wound healing; cancer; tumour; fibrosis; glaucoma; atherosclerosis;  
KW scleroderma; arthritis; cirrhosis; scar; diagnosis; therapy.

XX  
OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 28 /label= glycosylation

FT /note= "potential N-glycosylation site"

FT Modified-site 225 /label= glycosylation

FT /note= "potential N-glycosylation site"

XX  
PN W09638172-A1.

XX  
PD 05-DEC-1996.

XX  
XX 31-MAY-1996; 96WO-US08140.

XX  
XX 31-MAY-1996; 96WO-US08140.

XX  
PA (UYSF-) UNIV SOUTH FLORIDA.

XX  
PI Bradham DM, Grotendorst GR;

XX  
DR WPI; 1997-042659/04.

DR N-PSDB; AAT45360;  
XX N-PSDB; AAT58534.

XX  
XX  
PT Connective tissue growth factor coding sequence and protein - used  
PT in the treatment of proliferative disorders and to accelerate wound  
PT healing

PS  
XX Claim 19; Page 50-52; 76pp; English.

XX  
XX Novel human connective tissue growth factor (CTGF) (AAW09089) is a  
CC PGF-immunorelated protein that may play a significant role in the  
CC normal development, growth and repair of human tissue and probably  
CC functions as a growth factor in wound healing. CTGF may be involved  
CC in diseases in which there is an overgrowth of connective tissue  
CC cells, such as cancer, tumour formation and growth, fibrotic  
CC diseases (e.g. pulmonary fibrosis, kidney fibrosis, glaucoma) and  
CC atherosclerosis. Recombinant CTGF can be produced in transformed  
CC host cells utilising a cDNA clone isolated from a HUVEC library.  
CC It can be used to accelerate wound healing. CTGF inhibitors can be  
CC used to treat atherosclerosis and fibrotic diseases such as  
CC scleroderma, arthritis, liver cirrhosis, and scarring.

XX  
SQ Sequence 349 AA;

Query Match 100.0%; Score 948; DB 18; Length 349;  
Best Local Similarity 100.0%; Pred. No. 9.2e-86;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLETFGDPPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLKQSLCMV 60  
DB 180 aayrledtfgdpptmirancvlqttewsacsktcgmgistrvtndnascrlkqslcmv 239  
QY 61 RPEADLEENIKGKCIPTPKISKPIKFKELSGCTSMKTYRAKFCGVTGRCCTPHRTT 120  
DB 240 rpeadleenikgkciptpkiskpikfkfslsgctsmktyrakfcgvtgrcctphrtt 299  
QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 170  
DB 300 tlpvefkcpdgevmknmmfiktachyncpgdndifeslyyrkmygdma 349

#### RESULT 5

AAW11302  
ID AAW11302 standard; Protein; 349 AA.

XX  
AC AAW11302;

XX  
DT 18-MAR-1997 (first entry)

XX Connective tissue growth factor.

DE  
DE  
KW Connective tissue growth factor; CTGF; human; connective tissue cell;  
KW proliferative disease; platelet-derived growth factor; PDGF; development;  
KW tissue growth; repair; umbilical vein endothelial cell; HUVE cell;  
KW antibody; wound healing; cancer; fibrotic disease; atherosclerosis;  
KW inhibitor; protease degradation; growth factor; therapy.

XX  
OS Homo sapiens.

XX  
PN US5585270-A.

XX  
PD 17-DEC-1996.

XX  
PF 30-AUG-1991; 91US-0752427.

XX  
XX 30-AUG-1991; 91US-0752427.

XX  
PR 14-DEC-1993; 93US-0167628.

XX  
PR 10-FEB-1995; 95US-0386680.

XX  
PA (UYSF-) UNIV SOUTH FLORIDA.

XX  
PI Bradham DM, Grotendorst GR;

us-09-461-646-2\_copy\_180\_349.rag

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XX WPI; 1997-051180/05.  
 XX DR N-PSDB; AAT51234.  
 XX  
 XX New nucleic acid encoding connective tissue growth factor - useful  
 XX PT for accelerating wound healing, also for diagnosis and treatment of  
 XX PT proliferative disease  
 XX  
 XX Claim 9; Column 15-18; lpp: English.  
 XX  
 XX This sequence represents the human connective tissue growth factor  
 XX (CTGF). CTGF is related immunologically and biologically to  
 XX platelet-derived growth factor (PDGF), but is encoded by an unrelated  
 XX gene. CTGF is thought to play a significant role in the normal  
 XX development, growth, and repair of human tissue, similarly to PDGF. The  
 XX cDNA encoding this sequence was isolated by screening a cDNA library from  
 XX human umbilical vein endothelial (HUVE) cells with anti-PDGF antibodies.  
 XX CTGF can be used to accelerate wound healing. Also, elevated levels of  
 XX CTGF may be diagnostic of proliferative diseases involving outgrowth of  
 XX connective tissue cells, such as cancer, fibrotic disease and  
 XX atherosclerosis. All of these diseases can be treated with reagents  
 XX reactive with CTGF, such as antibodies (which can also serve as assay  
 XX reagents). Antisense nucleic acids, and ribozymes could also be used to  
 XX inhibit CTGF production. The advantage with using CTGF is that it is  
 XX more stable, and less susceptible to protease degradation than PDGF, and  
 XX other growth factors involved in wound healing. This is believed to be  
 XX due to the high Cys content.  
 XX  
 XX Sequence 349 AA:  
 SQ  
 Query Match 100.0%; Score 948; DB 18; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-86;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAYLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60  
 Db 180 aayrledtfpdpdmirancivqttewsacsktcgmgistrtvndnascrlkqslcmv 239  
 QY 61 RCEADLEENIKGKCIPTKIPKIFELSGCTSMKTYRAKFCGCTDGRCCPTPHRTT 120  
 Db 240 rpeadleenikgkciptkirkpikfsgctsmktyrakfcgctdgrccptphrtt 299  
 QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYPCGNDIFESLYYRKMVGMA 170  
 Db 300 tlpvefkcpdgevmkmmfiktachyncpgndifeslyyrkmygdma 349  
 RESULT 6  
 AAW62084 standard; Protein; 349 AA.  
 ID AAW62084  
 XX  
 XX AC AAW62084;  
 XX  
 XX DT 15-SEP-1998 (first entry)  
 XX  
 XX DE Human connective tissue growth factor.  
 XX  
 XX KW Human; connective tissue growth factor; CTGF; PDGF; diagnosis; cancer;  
 XX platelet derived growth factor; ameliorating cell proliferative disorder;  
 XX atherosclerosis; fibrotic disease.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN US5783187-A.  
 XX  
 XX PD 21-JUL-1998.  
 XX  
 XX PF 11-SEP-1996; 96US-0712302.  
 XX  
 XX PR 30-AUG-1991; 91US-0752427.  
 XX 14-DEC-1993; 93US-0167628.  
 XX 11-SEP-1996; 96US-0712302.  
 PR

XX (UYSF-) UNIV SOUTH FLORIDA.  
 XX PA Bradham DM, Grotendorst GR;  
 XX PI  
 XX WPI; 1998-426958/36.  
 XX DR N-PSDB; AAV38085.  
 XX  
 XX Ameliorating cell proliferative disorder associated with connective  
 XX tissue growth factor - comprises the administration of an antibody  
 XX which binds to connective tissue growth factor and not to  
 XX platelet-derived growth factor  
 XX  
 XX Example 6; Column 17-20; lpp: English.  
 XX  
 XX A method has been developed for ameliorating a cell proliferative  
 XX disorder associated with connective tissue growth factor (CTGF). The  
 XX method comprises the administration of an antibody or its fragment that  
 XX binds to CTGF and not to platelet-derived growth factor (PDGF), to the  
 XX site of the disorder. CTGF is related immunologically and biologically  
 XX to PDGF. The present sequence represents CTGF. The method is used to  
 XX treat conditions involving the overgrowth of connective tissue cells  
 XX such as cancer, atherosclerosis and other fibrotic diseases.  
 XX  
 XX Sequence 349 AA:  
 SQ  
 Query Match 100.0%; Score 948; DB 19; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-86;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAYLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60  
 Db 180 aayrledtfpdpdmirancivqttewsacsktcgmgistrtvndnascrlkqslcmv 239  
 QY 61 RCEADLEENIKGKCIPTKIPKIFELSGCTSMKTYRAKFCGCTDGRCCPTPHRTT 120  
 Db 240 rpeadleenikgkciptkirkpikfsgctsmktyrakfcgctdgrccptphrtt 299  
 QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYPCGNDIFESLYYRKMVGMA 170  
 Db 300 tlpvefkcpdgevmkmmfiktachyncpgndifeslyyrkmygdma 349  
 RESULT 7  
 AAY18361 standard; Protein; 349 AA.  
 ID AAY18361  
 XX  
 XX AC AAY18361;  
 XX  
 XX DT 20-AUG-1999 (first entry)  
 XX  
 XX DE Human connective tissue growth factor.  
 XX  
 XX KW CTGF; connective tissue growth factor; human; fibrotic disease;  
 XX cell proliferative disorder; atherosclerosis; diagnosis.  
 XX  
 XX OS Homo sapiens.  
 XX  
 XX PN US5916756-A.  
 XX  
 XX PD 29-JUN-1999.  
 XX  
 XX PF 20-JUN-1997; 97US-0880031.  
 XX  
 XX PR 14-DEC-1993; 93US-0167628.  
 XX 10-FEB-1995; 95US-0386680.  
 XX 11-SEP-1996; 96US-0712302.  
 XX 20-JUN-1997; 97US-0880031.  
 XX  
 XX PA (UYSF-) UNIV SOUTH FLORIDA.  
 XX PI Bradham DM, Grotendorst GR;



XX WPI; 1999-384720/32.  
 DR N-PSDB; AAX61317.  
 XX  
 XX Detecting cell proliferative disorders such as fibrotic disease and  
 PT atherosclerosis  
 PT  
 PS Disclosure; Column 15-18; 11pp; English.  
 XX  
 XX This sequence is the human connective tissue growth factor (CTGF).  
 CC The invention relates to a method of detecting a cell proliferative  
 CC disorder comprising comparing the level of CTGF in a sample against a  
 CC control, where an increase is indicative of a cell proliferative disorder  
 CC (fibrotic disease or atherosclerosis). The method is used to detect cell  
 CC proliferative disorders such as fibrotic disease and atherosclerosis.  
 XX  
 XX Sequence 349 AA;  
 SQ

Query Match 100.0%; Score 948; DB 20; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-86;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYLEDTFGDPTMIRANCLVQTTEWSACSKTCGMSGISTRTVNDNASCRLEKQSRLCMV 60  
 |||||  
 Db 180 aayrledtfgdptmirancivqttewsacsctcgmgistrvtndnascrlekqsrilmv 239  
 |||||

QY 61 RPEADLEENIKGKKIRTPKISKPIKFSLSGCTSMKTYRAKFCGCTDGRCTPHRTT 120  
 |||||  
 Db 240 rpeadleenikgkckirtpkiskpikfslsgctsmktyrakfcgctdgrctphrtt 299  
 |||||

QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPGDNDIFESLYYRKMVGMDMA 170  
 |||||  
 Db 300 tlpvefkcpdgevmknmmfiktachyncpgdndifeslyyrkmygdma 349  
 |||||

RESULT 8  
 AA081425  
 ID AA081425 standard; Protein: 349 AA.  
 XX  
 AC AA081425;  
 XX  
 DT 25-JAN-1999 (first entry)  
 XX  
 XX Connective tissue growth factor (CTGF).  
 DE  
 DE CTGF; connective tissue growth factor; bone formation; tissue; arthritis;  
 KW wound healing; cartilage formation; osteoporosis; osteoarthritis; burn;  
 KW osteochondritis; skeletal disorder; hypertrophic scar; protease; PDGF;  
 KW degradation; vascular hypertrophy; platelet derived growth factor.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT /note= "signal peptide"  
 FT Protein 22..349  
 FT /note= "mature protein"  
 XX  
 XX US5837258-A.  
 PN  
 XX  
 XX 17-NOV-1998.  
 PD  
 XX  
 XX 31-MAY-1996; 96US-0656393.  
 PF  
 XX  
 PR 31-MAY-1996; 96US-0656393.  
 PR 30-AUG-1991; 91US-0752427.  
 PR 14-DEC-1993; 93US-0167628.  
 PR 10-FEB-1995; 95US-0386680.  
 PR 02-JUN-1995; 95US-0459717.  
 XX  
 XX (UYMI-) UNIV MIAMI.  
 PA (UYSF-) UNIV SOUTH FLORIDA.  
 PA

XX Grotendorst GR;  
 PI  
 XX WPI; 1999-023382/02.  
 DR N-PSDB; AAY65380.  
 XX  
 XX Use of connective tissue growth factor - for inducing bone, tissue  
 PT or cartilage formation in a patient or for inducing wound healing  
 PT  
 PS Disclosure; Fig 1C; 30pp; English.  
 XX  
 XX This represents the amino acid sequence of connective tissue growth  
 CC factor (CTGF). This can be used in the method of the invention for  
 CC inducing bone or tissue formation that comprises administration to a  
 CC patient, a composition comprising CTGF and a carrier. CTGF can also be  
 CC used in a method for inducing wound healing. The methods can be used for  
 CC inducing bone, tissue or cartilage formation in disorders such as  
 CC osteoporosis, osteoarthritis or osteochondritis, arthritis, skeletal  
 CC disorders, hypertrophic scars, burns, vascular hypertrophy, or in wound  
 CC healing. The CTGF and functional fragments are more stable and less  
 CC susceptible to protease degradation than platelet derived growth factor  
 CC (PDGF) and other growth factors known to be involved in wound healing.  
 XX  
 XX Sequence 349 AA;  
 SQ

Query Match 100.0%; Score 948; DB 20; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-86;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYLEDTFGDPTMIRANCLVQTTEWSACSKTCGMSGISTRTVNDNASCRLEKQSRLCMV 60  
 |||||  
 Db 180 aayrledtfgdptmirancivqttewsacsctcgmgistrvtndnascrlekqsrilmv 239  
 |||||

QY 61 RPEADLEENIKGKKIRTPKISKPIKFSLSGCTSMKTYRAKFCGCTDGRCTPHRTT 120  
 |||||  
 Db 240 rpeadleenikgkckirtpkiskpikfslsgctsmktyrakfcgctdgrctphrtt 299  
 |||||

QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPGDNDIFESLYYRKMVGMDMA 170  
 |||||  
 Db 300 tlpvefkcpdgevmknmmfiktachyncpgdndifeslyyrkmygdma 349  
 |||||

RESULT 9  
 AA092939  
 ID AA092939 standard; Protein: 349 AA.  
 XX  
 AC AA092939;  
 XX  
 DT 08-NOV-2000 (first entry)  
 XX  
 XX Human connective tissue growth factor protein.  
 DE  
 DE Dermatological; antiarthritic; antiarteriosclerotic; antidiabetic;  
 KW nephrotropic; ophthalmological; hypotensive; cardiant; tranquilizer;  
 KW vulnery; antiinflammatory; human; connective tissue growth factor;  
 KW CTGF; extracellular matrix synthesis; collagen synthesis; antibody;  
 KW myofibroblast differentiation; antitense; fibroproliferative disease;  
 KW fibrosis; trauma; cancer; inflammation; diabetes; keloid.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200035936-A1.  
 XX  
 PD 22-JUN-2000.  
 XX  
 XX 14-DEC-1999; 99WO-US29652.  
 PF  
 XX  
 PR 14-DEC-1998; 98US-0112240.  
 PR 14-DEC-1998; 98US-0112241.  
 XX  
 XX (UYMI-) UNIV MIAMI.  
 PA  
 XX

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PI Grotendorst GR; 99WO-US29654.  
 XX 14-DEC-1999; 98US-0112240.  
 XX 14-DEC-1998; 98US-0112241.  
 DR N-PSDB; AA11278.  
 XX Fragment of connective tissue growth factor, useful for treating  
 XX fibroproliferative diseases or disorders, including kidney fibrosis,  
 PT scleroderma, arthritis, hypertrophic scarring, atherosclerosis, diabetic  
 PT nephropathy and retinopathy  
 XX Claim 2, 3; Fig 3A-B; 74pp; English.  
 PS This sequence represents a human connective tissue growth factor (CTGF)  
 XX polypeptide having the ability to induce extracellular matrix synthesis,  
 CC collagen synthesis and/or myofibroblast differentiation. The invention  
 CC relates to fragments of CTGF, especially those encoded by exons 2 and/or  
 CC 3, which contain the inductive activity. The protein and/or fragments  
 CC can be used to raise antibodies and the coding sequence can be used to  
 CC generate antisense oligonucleotides. The antibody or antisense sequence  
 CC against the CTGF sequence can be used in a method to treat a  
 CC CTGF-associated disease or disorder such as a fibroproliferative disease  
 CC or disorder, especially selected from kidney fibrosis, scleroderma,  
 CC pulmonary fibrosis, liver fibrosis, arthritis, hypertrophic scarring,  
 CC atherosclerosis, diabetic nephropathy and retinopathy, hypertension,  
 CC kidney disorders, angiogenesis-related disorders, skin fibrotic  
 CC disorders, and cardiovascular disorders. The disease or disorder can  
 CC also be selected from acute or repetitive traumas (including surgery or  
 CC radiation therapy, and fibrosis of organs), diseases caused by vascular  
 CC endothelial cell proliferation or migration (including cancers),  
 CC inflammatory bowel disease, Crohn's disease, joint inflammation,  
 CC interstitial disease, dermatological diseases, diabetes, and keloids.  
 XX Sequence 349 AA;  
 SQ

Query Match 100.0%; Score 948; DB 21; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-86;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 180 aayrledtfpdpmirancvlqttewsacsktcgmgistrvtndnasrlekqslrcmv 239  
 QY 61 RPEADLEENIKKGCIRTPKISKPIKPELSCGTSMTKTYRAKFCGVCVTDGRCCTPHRTT 120  
 DB 240 rpeadleenikkgcirtpkiskpikfelsgctsmkttyrakfcgvcctdgrcctphrtt 299  
 QY 121 TLPVFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIFESLYYRKMVGDMA 170  
 DB 300 tlpvfkcpdgevmknnmmfiktachyncpgdndifeslyyrkmygdma 349

RESULT 10  
 AAY92940  
 ID AAY92940 standard; Protein: 349 AA.  
 XX AC AAY92940;  
 XX DT 08-NOV-2000 (first entry)  
 XX DE Human connective tissue growth factor protein.  
 XX Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;  
 KW fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;  
 KW hypertrophic scarring; atherosclerosis; diabetic nephropathy; retinopathy;  
 KW hypertension; cardiovascular disorder; wound healing; bone repair.  
 XX Homo sapiens.  
 OS WO200035939-A2.  
 PN 22-JUN-2000.  
 XX PD

PF 14-DEC-1999; 99WO-US29654.  
 XX 14-DEC-1998; 98US-0112240.  
 PR 14-DEC-1998; 98US-0112241.  
 XX (UYMI-) UNIV MIAMI.  
 PA (FIBR-) FIBROGEN INC.  
 XX Grotendorst GR, Neff TB;  
 PI WPI: 2000-431568/37.  
 XX N-PSDB; AA11280.  
 DR New fragment of connective tissue growth factor (CTGF) polypeptide  
 XX having mitogenic activity, useful in wound healing, bone and tissue  
 PT repair -  
 XX Claim 2, 3; Fig 2A-B; 71pp; English.  
 PS This sequence represents a human connective tissue growth factor (CTGF)  
 XX polypeptide which has mitogenic activity. The protein can be used to  
 CC raise antibodies which specifically bind to CTGF and are used to treat  
 CC a CTGF-associated disease or disorder, e.g. a fibroproliferative  
 CC disease/disorder such as kidney fibrosis, scleroderma, pulmonary  
 CC fibrosis, liver fibrosis, arthritis, hypertrophic scarring,  
 CC atherosclerosis, diabetic nephropathy and retinopathy, hypertension,  
 CC kidney disorders, angiogenesis-related disorders, skin fibrotic  
 CC disorders, and cardiovascular disorders. The protein is also useful  
 CC in wound healing, bone and tissue repair.  
 XX Sequence 349 AA;  
 SQ

Query Match 100.0%; Score 948; DB 21; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-86;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLETFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSLRCMV 60  
 DB 180 aayrledtfpdpmirancvlqttewsacsktcgmgistrvtndnasrlekqslrcmv 239  
 QY 61 RPEADLEENIKKGCIRTPKISKPIKPELSCGTSMTKTYRAKFCGVCVTDGRCCTPHRTT 120  
 DB 240 rpeadleenikkgcirtpkiskpikfelsgctsmkttyrakfcgvcctdgrcctphrtt 299  
 QY 121 TLPVFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIFESLYYRKMVGDMA 170  
 DB 300 tlpvfkcpdgevmknnmmfiktachyncpgdndifeslyyrkmygdma 349

RESULT 11  
 AAY44755  
 ID AAY44755 standard; protein: 349 AA.  
 XX AC AAY44755;  
 XX DT 04-MAY-2000 (first entry)  
 XX DE Human connective tissue growth factor.  
 XX Connective tissue growth factor; CCN growth regulator; angiogenesis;  
 KW antiangiogenic; basic fibroblast growth factor; bFGF; neovascular;  
 KW endothelial cell proliferation; retinal; haemangioma; leukaemia;  
 KW metastasis; psoriasis; tumour; glaucoma; diabetic retinopathy; arthritis;  
 KW endometriosis; Insulin-like growth factor-binding domain; IGF;  
 KW von Willebrand factor type C repeat; Thrombospondin type 1 domain;  
 KW C-terminal cysteine knot profile; CTCK-2; human.  
 XX Homo sapiens.  
 OS WO200005356-A1.  
 PN 03-FEB-2000.  
 XX PD

PR	10-FEB-1995;	95US-0386680.
PR	30-AUG-1991;	91US-0752427.
PR	11-SEP-1996;	96US-0712302.
XX		
XX	(UYSF-) UNIV SOUTH FLORIDA.	
XX		
PI	Grotendorst GR, Bradham DM;	
XX		
PI	WPI; 2001-210379/21.	
DR	N-PSDB; AAF59954.	
XX		
XX		
PT	Producing connective tissue growth factor involves transforming a host	
PT	cell with polynucleotide encoding the growth factor and growing the	
PT	cell under optimum conditions so that the polynucleotide is expressed	
XX		
XX		
PS	Claim 1; Column 17-20; 11pp; English.	
XX		
CC	The invention relates to a method for the recombinant production of	
CC	human connective tissue growth factor (CTGF; AAB060664), involving	
CC	transforming a prokaryotic or eukaryotic host cell with an expression	
CC	construct comprising the CTGF cDNA sequence (AAF59954) or a fragment	
CC	thereof, and culturing the host cell under conditions suitable for the	
CC	expression of CTGF. CTGF is a mitogen and chemotactic agent for	
CC	connective tissue cells and plays a significant role in normal	
CC	development, growth and repair of human tissues. It is useful as a	
CC	therapeutic for accelerating wound healing and promoting normal healing	
CC	mechanisms and may therefore be used in the treatment of e.g., burns.	
CC	CTGF is also useful as a diagnostic reagent for diagnosing pathological	
CC	states in a patient suspected of having a disease characterised by a	
CC	disorder of cellular proliferation. The present sequence represents	
CC	human CTGF.	
XX		
SQ	Sequence. 349 AA;	
	Query Match 100.0%; Score 948; DB 22; Length 349;	
	Best Local Similarity 100.0%; Pred. No. 9.2e-86;	
	Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 AAYRLEDTFGPDMTRANCLVQTTEWSACSKYTCGNGISTRTVTNDNASCRLEKQSLCMV 60	
Db	180 aayrledtfgdpdmtrancvlgttewsacsxktcgmgistrtvtndnascrlekqslcmv 239	
QY	61 RPEADLEENIKKGKKCIRTPKISKIPKFELSGCTSMKTYRAKTCGVCTDGRCCCTPHRTT 120	
Db	240 rpeadleenikgkkcirtpkiskipkfelsgcsmktyraktcgvctdgrccctphrtt 299	
QY	121 TLPVEFKCPDGVEYKNNMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 170	
Db	300 tlpvefkcpdgveymknmmfiktachyncpgdndifeslyrkmygdma 349	
RESULT	13	
AAB48831	ID	
XX	AAB48831 standard; Protein; 349 AA.	
XX		
AC	AAB48831;	
XX		
DT	09-MAR-2001 (first entry)	
XX		
DE	Human connective tissue growth factor (CTGF).	
XX		
KW	Human; connective tissue growth factor; CTGF; PDGF-like activity;	
KW	platelet-derived growth factor; transforming growth factor-beta;	
KW	TGF-beta; mitogenic; proliferative; chemotactic; wound healing;	
KW	vulnerary; endothelial cell; fibroblast.	
OS	Homo sapiens.	
XX		
PN	US6149916-A.	
XX		
PD	21-NOV-2000.	

```

12-JUN-1998; 98US-0097179.
14-DEC-1993; 93US-0167628.
10-FEB-1995; 95US-0396680.
11-SEP-1996; 96US-0712302.
30-AUG-1991; 91US-0752427.
(UYSF-) UNIV SOUTH FLORIDA.
Bradham DM, Grotendorst GR;
N-PSDB; AAC87517.
Accelerating wound healing or stimulating growth of connective tissue
cells involves contacting the site of a wound or cells with a
composition comprising purified connective tissue growth factor and
transforming growth factor beta
Claim 1: Column 17-20; lipp; English.
The invention relates to methods of accelerating wound healing in a
patient. One method involves contacting the site of the wound with a
composition comprising purified connective tissue growth factor
(CTGF; AAB4831) and transforming growth factor beta (TGF-beta), which
stimulates the production of CTGF in vivo. Another method involves
stimulating the growth of connective tissue cells by contacting the
cells with CTGF or an active fragment thereof. CTGF is produced by
endothelial and fibroblastic cells, both of which are present at the
site of a wound, and is mitogenic and chemotactic for connective tissue
cells. It has biologically similar activity to PDGF (platelet-derived
growth factor), and is also immunologically related to it, but it is
the product of a distinct gene. CTGF is useful for accelerating wound
healing by stimulating the growth of connective tissue cells. CTGF, or
its functional fragments, is more stable and less susceptible to be
protease degradation than PDGF and other growth factors known to be
involved in wound healing. The present sequence represents human CTGF.
Sequence 349 AA:
Query Match 100.0%; Score 948; DB 22; Length 349;
Best Local Similarity 100.0%; Pred. No. 9,2e-86;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps
0
Qy 1 AAYRLDTFGPDTMIRANCLVQTTWWSACSKTCGNGISTRYTNDNASCRLEKQSRLCMV 60
Db 180 aayrledtfgpdtmiranclvqtwwsacsktcgngistrvndnascrlekqsrldmv 239
Qy 61 RPEADLEENIKKGGKIRTPKTSKPKFELSCTSMKTYRAKFCGCVTDGRCCCTPHRTT 120
Db 240 rpceadleenlkkggkrlrtpktskpkfelsctsmktyrakfcgvtddgrccctphrtt 299
Qy 121 TLVPVEFKCPDGEVMKNNMFKTKTCACHYNCPGDNDIFESLYYRKMYGDMA 170
Db 300 tlvpvefkcpdgevnmknnmfktktcachyncpgdndifeslyyrkmygdma 349
RESULT 14
AAY24379
ID AAY24379 standard; Protein; 347 AA.
XX
AC AAY24379;
XX
XX 17-SEP-1999 (first entry)
XX
XX Rat connective tissue growth factor.
XX Human; monoclonal antibody; connective tissue growth factor; CTGF;
XX cell proliferation disorder; fibrosis; liver cirrhosis; nephritis;
XX skin ulcer; keloid; rheumatoid arthritis; hepatitis; cancer;
XX rheumatic vascular inflammation.

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XX 18-JAN-1991; 91US-0642991.
PR 10-JAN-1992; 92US-0816270.
XX
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX PI Brunner AM, Chinn J, Neubauer MG, Purchio AF;
XX
XX DR WPI; 1992-243508/30.
XX DR N-PSDB; AAQ26422.
XX
XX PT TGF-beta induced gene family - encodes proteins involved in
XX PT growth and differentiation effects of TGF-beta-1
XX PS
XX PS Claim 3; Fig 2; 35pp; English.
XX
XX CC The protein sequence was deduced from the DNA sequence obt'd. by
XX CC screening a cDNA library made from AKR-2B mouse cells induced with
XX CC TGF-beta1 and cyclohexamide with two probes from untreated AKR-2B
XX CC mRNA and AKR-2B mRNA from cells treated with cyclohexamide and TGF-
XX CC beta1. The proteins encoded by hybridising colonies (beta-IG-M1 and
XX CC beta-IG-M2) contain 38 Cys residues and are induced by TGF-beta1.
XX CC Beta-IG-M2 displays 50 percent homology to the CEF-10 protein
XX CC induced by v-src in chicken embryo fibroblasts. Residues 52-59
XX CC of beta-IG-M2 conform to the GCGCCXXC motif reported in the
XX CC amino half of insulin-like growth factor (IGF) binding proteins.
XX CC The C-terminal Cys rich region of beta-IG-M1, -M2 and CEF-10 contain
XX CC an amino acid sequence with strong homology to a motif found near the
XX CC C-terminal of the malarial circumsporozoite (CS) protein, which is
XX CC highly conserved among all species of malarial parasites sequenced
XX CC to date (designated region II). This motif is also found in
XX CC other proteins which have cell adhesive properties that mediate
XX CC cell-cell and cell-extracellular matrix interactions, such as
XX CC properdin, thrombospondin, and TRAP. The proteins encoded by
XX CC TGF-beta induced genes are likely to be involved in mediation of
XX CC the biological effects of TGF-beta relating to cell growth and
XX CC differentiation. See also AAR25565.
XX
XX SQ Sequence 348 AA;

Query Match 97.7%; Score 926; DB 13; Length 348;
Best Local Similarity 95.9%; Pred. No. 1.4e-83;
Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGDPDMIRANCLVQTTENSACSKTCGMGISTRTVNDNASCRLEKOSRLCMV 60
Db ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
179 aayrledtfgdpdmirancvlqtewsacsktcgmgistrtvndntfcrlekgsrlcmv 238

QY 61 RPCADLEENIKGKCKIRTPKISKPIKFSLGCTSMKTYRAKFCGVCTDGRCCCTPHRTT 120
Db ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
239 rpceadleenikgkckirtpkiakpvkfslgctsvktyrakfcgvctdgrccctphrtt 298

QY 121 TLPVFEFKCPDGEVMMKMMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 170
Db ||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
299 tlpvfefkcpdgeimkmmfiktachyncpgdndifeslyyrkmygdma 348
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Job time: 2504 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2001, 22:06:59 ; Search time 72.24 Seconds  
(without alignments)  
48.455 Million cell updates/sec

Title: US-09-461-646-2\_COPY\_180\_349

Perfect score: 948

Sequence: 1 AAYRLEDTFGPDPTMIRAN.....PGDNDFESLYRYKMYGDMA 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	100.0	348	1	US-08-468-847B-14
2	948	100.0	349	1	US-08-167-628-2
3	948	100.0	349	1	US-08-386-680-2
4	948	100.0	349	1	US-08-459-717-2
5	948	100.0	349	1	US-08-712-302-2
6	948	100.0	349	2	US-08-880-031-2
7	948	100.0	349	3	US-09-054-368-2
8	948	100.0	349	4	US-09-097-179-2
9	948	100.0	349	4	US-09-054-274-2
10	948	100.0	349	4	US-09-080-715-2
11	948	100.0	349	4	US-09-056-704-2
12	948	100.0	349	5	PCT-US96-08140-2
13	926	97.7	348	1	US-08-468-847B-15
14	540.5	57.0	351	1	US-08-468-847B-16
15	515	54.3	357	1	US-08-468-847B-17
16	487.5	51.4	379	1	US-08-468-847B-11
17	479.5	50.6	375	1	US-08-468-847B-13
18	469.5	49.5	374	1	US-08-468-847B-12
19	468.5	49.4	375	2	US-08-459-101A-2
20	141	14.9	24	2	US-08-908-526-20
21	101.5	10.7	807	1	US-07-862-021B-10
22	101.5	10.7	807	1	US-08-313-288B-10
23	101.5	10.7	807	5	PCT-US93-03164-10
24	99	10.4	18	2	US-08-908-526-15
25	96	10.1	464	3	US-08-957-063-6
26	96	10.1	664	3	US-08-957-063-18
27	95	10.0	423	2	US-08-760-797A-1

Sequence 1, Appli  
Sequence 3, Appli  
Sequence 16, Appl  
Sequence 183, App  
Sequence 13, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 8, Appli  
Sequence 34, Appl  
Sequence 34, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 18, Appl  
Sequence 14, Appl  
Sequence 14, Appl

#### ALIGNMENTS

RESULT 1  
US-08-468-847B-14  
; Sequence 14, Application US/08468847B  
; Patent No. 5780263  
; GENERAL INFORMATION:  
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.  
; TITLE OF INVENTION: Human CCN-Like Growth Factor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKT FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,847B  
; FILING DATE: 6 June 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-442  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 348 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-08-468-847B-14

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Best Local Similarity 100.0%; Pred. No. 4.3e-83;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Tue Aug 21 08:16:54 2001

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QY 61 RPEADLEENIKGKKICIRTPKISKPIKFKELSGCTSMKTYRAKFCGVCCTDGRCCCTPHRTT 120  
Db 239 RPEADLEENIKGKKICIRTPKISKPIKFKELSGCTSMKTYRAKFCGVCCTDGRCCCTPHRTT 298  
QY 121 TLPVEFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIFESLYYRKMVGMDMA 170  
Db 299 TLPVEFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIFESLYYRKMVGMDMA 348

RESULT 2  
US-08-167-628-2  
; Sequence 2, Application US/08167628  
; Patent No. 5408040  
; GENERAL INFORMATION:  
; APPLICANT: Grotendorst, Gary R.  
; APPLICANT: Bradham Jr., Douglas M.,  
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Jubas & Lubitz  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/167,628  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/752,427  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wetherell, Jr. Ph.D., John W.  
; REGISTRATION NUMBER: 31,678  
; REFERENCE/DOCKET NUMBER: PD-1294  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-455-5110  
; TELEFAX: 619-455-5110  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 349 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-167-628-2

Query Match 100.0%; Score 948; DB 1; Length 349;  
Best Local Similarity 100.0%; Pred. No. 4.3e-83;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 RPEADLEENIKGKKICIRTPKISKPIKFKELSGCTSMKTYRAKFCGVCCTDGRCCCTPHRTT 120  
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RESULT 3  
US-08-386-680-2  
; Sequence 2, Application US/08386680  
; Patent No. 5585270  
; GENERAL INFORMATION:  
; APPLICANT: Grotendorst, Gary R.  
; APPLICANT: Bradham Jr., Douglas M.,  
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Spensley Horn Jubas & Lubitz  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/386,680  
; FILING DATE: 10-FEB-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/167,628  
; FILING DATE:  
; APPLICATION NUMBER: US/07/752,427  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wetherell, Jr. Ph.D., John W.  
; REGISTRATION NUMBER: 31,678  
; REFERENCE/DOCKET NUMBER: PD-1294  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-455-5110  
; TELEFAX: 619-455-5110  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 349 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-386-680-2

Query Match 100.0%; Score 948; DB 1; Length 349;  
Best Local Similarity 100.0%; Pred. No. 4.3e-83;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRCLMV 60  
Db 180 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRCLMV 239  
QY 61 RPEADLEENIKGKKICIRTPKISKPIKFKELSGCTSMKTYRAKFCGVCCTDGRCCCTPHRTT 120  
Db 240 RPEADLEENIKGKKICIRTPKISKPIKFKELSGCTSMKTYRAKFCGVCCTDGRCCCTPHRTT 299  
QY 121 TLPVEFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIFESLYYRKMVGMDMA 170  
Db 300 TLPVEFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIFESLYYRKMVGMDMA 349

RESULT 4  
US-08-459-717-2  
; Sequence 2, Application US/08459717  
; Patent No. 5770209  
; GENERAL INFORMATION:  
; APPLICANT: Grotendorst, Gary R.  
; APPLICANT: Bradham Jr., Douglas M.,  
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:



Query Match 100.0%; Score 948; DB 1; Length 349;

Best Local Similarity 100.0%; Pred. No. 4.3e-83;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/880,031  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/157,628  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weatherell, Jr. Ph.D. John W.



```
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham, Jr., Douglas M.
; TITLE OF INVENTION: METHODS OF IDENTIFYING A COMPOSITION
; TITLE OF INVENTION: THAT ALTERS CONNECTIVE TISSUE GROWTH
; TITLE OF INVENTION: FACTOR EXPRESSION (Amended)
; FILE REFERENCE: 07414/003004
; CURRENT APPLICATION NUMBER: US/09/054,274
; CURRENT FILING DATE: 1998-04-02
; EARLIER APPLICATION NUMBER: 08/386,680
; EARLIER FILING DATE: 1995-02-10
; EARLIER APPLICATION NUMBER: 08/459,717
; EARLIER FILING DATE: 1995-06-02
; EARLIER APPLICATION NUMBER: 08/167,628
; EARLIER FILING DATE: 1993-12-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-054-274-2

Query Match      100.0%; Score 948; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.3e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGGMGISTRTVNDNASCRLKQSLCMV 60
Db 180 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGGMGISTRTVNDNASCRLKQSLCMV 239
QY 61 RPCEADLEENIKGKKCIRTTPKISKPIKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 120
Db 240 RPCEADLEENIKGKKCIRTTPKISKPIKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 299
QY 121 TLPVEFKCPDGEVKNMFMFKTCACHYNCPGDNDIFESLYYRKMVGMDA 170
Db 300 TLPVEFKCPDGEVKNMFMFKTCACHYNCPGDNDIFESLYYRKMVGMDA 349

RESULT 10
US-09-080-715-2
; Sequence 2, Application US/09080715
; Patent No. 6190884
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr. Ph.D., John W.
; REGISTRATION NUMBER: 31,678
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; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-080-715-2
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Query Match      100.0%; Score 948; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.3e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGGMGISTRTVNDNASCRLKQSLCMV 60
Db 180 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGGMGISTRTVNDNASCRLKQSLCMV 239
QY 61 RPCEADLEENIKGKKCIRTTPKISKPIKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 120
Db 240 RPCEADLEENIKGKKCIRTTPKISKPIKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 299
QY 121 TLPVEFKCPDGEVKNMFMFKTCACHYNCPGDNDIFESLYYRKMVGMDA 170
Db 300 TLPVEFKCPDGEVKNMFMFKTCACHYNCPGDNDIFESLYYRKMVGMDA 349
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RESULT 11
US-09-056-704-2
; Sequence 2, Application US/09056704
; Patent No. 6232064
; GENERAL INFORMATION:
; APPLICANT: University of South Florida
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham, Jr., Douglas M.
; TITLE OF INVENTION: METHODS OF DIAGNOSING A PATHOLOGY
; TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE
; TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
; TITLE OF INVENTION: TISSUE GROWTH FACTOR (Amended)
; FILE REFERENCE: 07414/003002
; CURRENT APPLICATION NUMBER: US/09/056,704
; CURRENT FILING DATE: 1998-03-03
; EARLIER APPLICATION NUMBER: 08/386,680
; EARLIER FILING DATE: 1995-02-10
; EARLIER APPLICATION NUMBER: 08/459,717
; EARLIER FILING DATE: 1995-06-02
; EARLIER APPLICATION NUMBER: 08/167,628
; EARLIER FILING DATE: 1993-12-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-056-704-2
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Query Match      100.0%; Score 948; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 4.3e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGGMGISTRTVNDNASCRLKQSLCMV 60
Db 180 AAYRLEDTFGPDTMIRANCLVQTTEWSACSKTCGGMGISTRTVNDNASCRLKQSLCMV 239
QY 61 RPCEADLEENIKGKKCIRTTPKISKPIKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 120
Db 240 RPCEADLEENIKGKKCIRTTPKISKPIKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 299
QY 121 TLPVEFKCPDGEVKNMFMFKTCACHYNCPGDNDIFESLYYRKMVGMDA 170
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; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-442  
; TELEPHONE: 201-994-1700  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 351 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-08-468-847B-16

Query Match 57.0%; Score 540.5; DB 1; Length 351;  
Best Local Similarity 59.9%; Pred. No. 3.3e-44;  
Matches 94; Conservative 22; Mismatches 40; Indels 1; Gaps 1;  
QY 1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGGMGISTRTVNDNASCRLEKQSRCLMV 60  
Db 183 AAYRQEAATLGDVSDSSANCIEQTTEWSACSKCGMGFSTRVNNRQCEMVKQTRLCMM 242  
QY 61 RPEADLEENIKKGGKCIPTPKSKPKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 120  
Db 243 RPCNEE-EPSSDKKGGKCIPTPKSKPKFELSGCTSMKTYRAKFCGVTGRCCTPHRTT 1  
QY 121 TLPVEFKCPDGEVYKKNMFIKTCACHYNCPGDNDIF 157  
Db 302 TIQVEFKCPDGEVYKKNMFIKTCACHYNCPGDNDIF 338

RESULT 15  
US-08-468-847B-17  
; Sequence 17, Application US/08468847B  
; Patent No. 5780263  
; GENERAL INFORMATION:  
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.  
; TITLE OF INVENTION: Human CCN-Like Growth Factor  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLIAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,847B  
; FILING DATE: 6 June 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-442  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 357 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-08-468-847B-17

Query Match 54.3%; Score 515; DB 1; Length 357;  
Best Local Similarity 54.4%; Pred. No. 9.2e-42;  
Matches 93; Conservative 25; Mismatches 51; Indels 2; Gaps 2;  
QY 1 AAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGGMGISTRTVNDNASCRLEKQSRCLMV 60  
Db 187 AAYRPEATLGLVEVSDSSVNCIEQTTEWSACSKCGMGFSTRVNNRQCEMLKQTRLCMV 246  
QY 61 RPEADLEE-NIKKGGKCIPTPKSKPKFELSGCTSMKTYRAKFCGVTGRCCTPHRT 119  
Db 247 RPECQEPEQPTDKKGGKCLRTKSLKAIHLQFNKCTSLHTYKPRFCGVCSDGRCCTPHNT 306  
QY 120 TLPVEFKCPDGEVYKKNMFIKTCACHYNCPGDNDIF-ESLYYRKMVGDM 169  
Db 307 KTQAEFQCSPGQIVKKPVAVIGTCTCTNCPKNNEAFLOELELKTTRGKM 357

Search completed: August 20, 2001, 22:47:51  
Job time: 2452 sec

us-09-461-646-2\_copy\_180\_349.ra1

Tue Aug 21 08:16:54 2001

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Tue Aug 21 08:16:54 2001

gene novH protein - human  
C:Species: Homo sapiens (man)  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 05-Nov-1999  
C:Accession: I38069  
R:Martinierie, C.; Huff, V.; Joubert, I.; Badzioch, M.; Saunders, G.; Strong, L.; Perb  
Oncogene 9, 2729-2732, 1994  
A:Title: Structural analysis of the human nov proto-oncogene and expression in Wilms  
Cell Growth Differ. 2, 225-233, 1991  
A:Reference number: 138069; MUID:94336229  
A:Accession: I38069  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-357 <RES>  
A:Cross-references: EMBL:X78351; NID:g587422; PIDN:CAA55146.1; PID:g825696  
C:Genetics:  
A:Gene: novH  
A:Introns: 28/3; 104/1; 188/1; 259/3  
A:Superfamily: thrombospondin type 1 repeat homology  
F:203-250/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 97.7%; Score 926; DB 2; Length 348;  
Best Local Similarity 95.9%; Pred. No. 1.2e-73;  
Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AAYRLEDFGPDPTMIRANCLVQTTWSSACSKTCGMISTRVNDNASCRLKQSLCMV 60  
DB 179 AAYRLEDFGPDPTMIRANCLVQTTWSSACSKTCGMISTRVNDNASCRLKQSLCMV 238  
QY 61 RCEADLEENIKKKKICRTPKISKPIKFSLSGCTSMKTYRAKFCGCTDGRCTPHRTT 120  
DB 239 RCEADLEENIKKKKICRTPKIAKVPKFSLSGCTSVKTYRAKFCGCTDGRCTPHRTT 298  
QY 121 TLPVEFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIFESLYRKMVGDM 170  
DB 299 TLPVEFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIFESLYRKMVGDM 348

RESULT 3  
S20078  
NOV protein - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: S20078  
R:Joliot, V.; Martinierie, C.; Dambrine, G.; Plassiart, G.; Brisac, M.; Crochet, J.; Perb  
Mol. Cell. Biol. 12, 10-21, 1992  
A:Title: Proviral rearrangements and overexpression of a new cellular gene (nov) in myel  
A:Reference number: S20078; MUID:92107157  
A:Accession: S20078  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-351 <JOL>  
A:Cross-references: EMBL:X59284; NID:g63702; PIDN:CAA41975.1; PID:g63703  
C:Genetics:  
A:Gene: NOV

Query Match 57.0%; Score 540.5; DB 2; Length 351;  
Best Local Similarity 59.9%; Pred. No. 5.4e-40;  
Matches 94; Conservative 22; Mismatches 40; Indels 1; Gaps 1;  
QY 1 AAYRLEDFGPDPTMIRANCLVQTTWSSACSKTCGMISTRVNDNASCRLKQSLCMV 60  
DB 183 AAYRLEATLGIDVSDSSANCIEQTTWSSACSKTCGMISTRVNDNASCRLKQSLCMV 242  
QY 61 RCEADLEENIKKKKICRTPKISKPIKFSLSGCTSMKTYRAKFCGCTDGRCTPHRTT 120  
DB 243 RCPENE-EFSDKKGKKICRTPKISKPIKFSLSGCTSMKTYRAKFCGCTDGRCTPHRTT 301  
QY 121 TLPVEFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIF 157  
DB 302 TIQVEFRCPQGGFLKKPKMMLINTVCVCHGNCPOSNAF 338

RESULT 4  
I38069

Query Match 54.3%; Score 515; DB 2; Length 357;  
Best Local Similarity 54.4%; Pred. No. 9.2e-38;  
Matches 93; Conservative 25; Mismatches 51; Indels 2; Gaps 2;  
QY 1 AAYRLEDFGPDPTMIRANCLVQTTWSSACSKTCGMISTRVNDNASCRLKQSLCMV 60  
DB 187 AAYRLEATLGVEVSDSSVNCIEQTTWSSACSKTCGMISTRVNDNASCRLKQSLCMV 246  
QY 61 RCEADLEENIKKKKICRTPKISKPIKFSLSGCTSMKTYRAKFCGCTDGRCTPHRTT 119  
DB 247 RCPQEPDPTDKKGGKCLRTKKSILKAIHLQFNKTSLSHTYKPRFCGCGSDGRCCTPHNT 306  
QY 120 TLPVEFKCPDGEVMMKNNMFIKTCACHYNCPGDNDIF-ESLYRKMVGDM 169  
DB 307 KITQAEFCQCGQIVKPKVMVIGTCTCHTNCPCNNKNEAFLELELKTTRGKM 357

RESULT 5  
A35669  
gene CYR61 protein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Sep-1990 #sequence\_revision 18-Nov-1992 #text\_change 05-Nov-1999  
C:Accession: A35669; I48319; S16446  
R:O'Brien, T.P.; Yang, G.P.; Sanders, L.; Lau, L.F.  
Mol. Cell. Biol. 10, 3569-3577, 1990  
A:Title: Expression of cyr61, a growth factor-inducible immediate-early gene.  
A:Reference number: A35669; MUID:90287146  
A:Accession: A35669  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-379 <OAB>  
A:Cross-references: GB:M32490; NID:g192909; PIDN:AAA37512.1; PID:g309206  
A:Note: the authors translated the codon GAT for residue 337 as Gln  
R:Latinkic, B.V.; O'Brien, T.P.; Lau, L.F.  
Nucleic Acids Res. 19, 3261-3267, 1991  
A:Title: Promoter function and structure of the growth factor-inducible immediate ear  
A:Reference number: I48319; MUID:91288203  
A:Accession: I48319  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-379 <RES>  
A:Cross-references: EMBL:X56790; NID:g50632; PIDN:CAA40109.1; PID:g50633  
A:Note: the authors did not translate the codon for residue 108  
A:Note: the authors translated the codon GAT for residue 337 as Gln  
C:Genetics:  
A:Gene: CYR61  
A:Introns: 21/3; 93/1; 208/1; 279/3  
A:Superfamily: von Willebrand factor type C repeat homology  
F:99-166/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 51.4%; Score 487.5; DB 2; Length 379;  
Best Local Similarity 49.4%; Pred. No. 2.4e-35;









[illegible]

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 20, 2001, 22:47:55 ; Search time 57.66 Seconds  
(without alignments)  
100.996 Million cell updates/sec

Title: US-09-461-646-2\_COPY\_180\_349

Perfect score: 948

Sequence: 1 AYRLIEDFGDPTMIRANCR.....PGDNDFESLYRYKMYGDMA 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	948	100.0	349	1	CTGF_HUMAN
2	929	98.0	349	1	CTGF_PIG
3	926	97.7	348	1	CTGF_MOUSE
4	906	95.6	349	1	CTGF_BOVIN
5	541.5	57.1	353	1	NOV_COTJA
6	540.5	57.0	351	1	NOV_CHICK
7	518.5	54.7	343	1	NOV_XENLA
8	515	54.3	357	1	NOV_HUMAN
9	512.5	54.1	354	1	NOV_MOUSE
10	487.5	51.4	379	1	CYR6_MOUSE
11	485.5	51.2	381	1	CYR6_HUMAN
12	479.5	50.6	375	1	CE10_CHICK
13	101.5	10.7	465	1	NRTX_CHICK
14	101.5	10.7	807	1	FSPO_RAT
15	99	10.4	803	1	FSPO_XENLA
16	97	10.2	4753	1	LRP_CAEEL
17	94	9.9	463	1	NRTX_MOUSE
18	94	9.9	464	1	NRTX_HUMAN
19	92	9.7	1205	1	ATS2_BOVIN
20	89.5	9.4	388	1	CSP_PLARE
21	89.5	9.4	1178	1	TSP2_CHICK
22	89	9.4	1173	1	TSP1_XENLA
23	88.5	9.3	105	1	MT1_TETPI
24	88.5	9.3	464	1	GDNR_HUMAN
25	88.5	9.3	469	1	GDNR_CHICK
26	88.5	9.3	810	1	NELL_HUMAN
27	87.5	9.2	412	1	CSP_PLAFA
28	87.5	9.2	424	1	CSP_PLAFT
29	87.5	9.2	442	1	CSP_PLAFW
30	87.5	9.2	1211	1	ATS2_HUMAN
31	87	9.2	732	1	2267_HUMAN
32	87	9.2	837	1	MUCL_RAT
33	87	9.2	1170	1	TSP1_HUMAN

34	86	9.1	1170	1	TSP1_BOVIN
35	86	9.1	1170	1	TSP1_MOUSE
36	85	9.0	151	1	KR2C_SHEEP
37	84.5	8.9	397	1	CSP_PLAFO
38	84	8.9	1170	1	TSP2_BOVIN
39	84	8.9	2146	1	INSR_DROME
40	83.5	8.8	810	1	NELL_RAT
41	83.5	8.8	1584	1	BAIL_HUMAN
42	82.5	8.7	934	1	CO6_HUMAN
43	82	8.6	4289	1	TENX_HUMAN
44	81.5	8.6	4655	1	LRP2_HUMAN
45	81	8.5	610	1	TOH2_CAEEL

#### ALIGNMENTS

RESULT 1	
CTGF_HUMAN	
ID	CTGF_HUMAN
AC	STANDARD; PRT; 349 AA.
DT	01-DEC-1992 (Rel. 24, Created)
DT	01-DEC-1992 (Rel. 24, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
GN	CTGF.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-Umbilical vein endothelial cells;
RX	MEDLINE=91373462; PubMed=1654338;
RA	Bradham D.M., Igarashi A., Potter R.L., Grotendorst G.R.;
RT	"Connective tissue growth factor: a cysteine-rich mitogen secreted by
RT	human vascular endothelial cells is related to the SRC-induced
RL	immediate early gene product CEF-10.";
RL	J. Cell Biol. 114:1285-1294(1991).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE-Umbilical vein endothelial cells;
RX	MEDLINE=93187114; PubMed=1293144;
RA	Igarashi A., Bradham D.M., Okochi H., Grotendorst G.R.;
RT	"Connective tissue growth factor.";
RL	J. Dermatol. 19:642-643(1992).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=97207446; PubMed=9054739;
RA	Oemar B.S., Werner A., Garnier J.M., Do D.D., Godoy N., Nauck M.,
RA	Marz W., Rupp J., Pech M., Luescher T.F.;
RT	"Human connective tissue growth factor is expressed in advanced
RT	atherosclerotic lesions.";
RL	Circulation 95:931-939(1997).
CC	-!- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY
CC	HUMAN VASCULAR ENDOTHELIAL CELLS. THIS IMMEDIATE-EARLY PROTEIN
CC	MAY BIND ONE OF THE PDGF CELL SURFACE RECEPTORS.
CC	-!- SUBUNIT: MONOMER.
CC	-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC	SHORT FORM; SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.
CC	-!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC	PROTEIN FAMILY. CEF-10/CYR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.
CC	-!- SIMILARITY: CONTAINS 1 WVFC DOMAIN.
CC	-!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE DOMAIN (CTCK).
CC	-----
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----

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Query Match          100.0%; Score 948; DB 1; Length 343;
Best Local Similarity 100.0%; Pred. No. 1.le-77;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1  AAYRLEDFGDDPTMIRANCLVOTTWWSACSKTCGMSGISTRTVNDNASCRLKQSRLCMV 60
180 AAYRLEDFGDDPTMIRANCLVOTTWWSACSKTCGMSGISTRTVNDNASCRLKQSRLCMV 239
61 RCEADLEENIKKKGKICIRPKISKIPKELSGCTSMKTYRAKFCGVCYDGRCTPHRTT 120
240 RCEADLEENIKKKGKICIRPKISKIPKELSGCTSMKTYRAKFCGVCYDGRCTPHRTT 299
121 TLPVEFKCPDGEVWKKNNMFKTCACHYNCPGDNDIFESLYYRKNMYGDMA 170
300 TLPVEFKCPDGEVWKKNNMFKTCACHYNCPGDNDIFESLYYRKNMYGDMA 349

RESULT 2
CTGF_PIG STANDARD; PRT; 349 AA.
CTGF_PIG
AC 019113;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last sequence update)
CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
CTGF
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
NRN
SEQUENCE FROM N.A.
RP
TISSUE=Uterus;
RC
RX MEDLINE=97390475; PubMed=9242708;
RA Brigsstock D.R., Steffen C.L., Kim G.Y., Vegunta R.K., Diehl J.R.,
Harding P.A.;
RA "Purification and characterization of novel heparin-binding growth
RT factors in uterine secretory fluids. Identification as heparin-
RT regulated Mr 10,000 forms of connective tissue growth factor.";
RL J. Biol. Chem. 272:20275-20282(1997).

```

1] SEQUENCE FROM N.A.  
 MEDLINE=91363290; PubMed=1888698;  
 Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;  
 "Structure, mapping, and expression of fisp-12, a growth factor-  
 inducible gene encoding a secreted cysteine-rich protein.";  
 Cell Growth Differ. 2:225-233(1991).  
 2] SEQUENCE FROM N.A.  
 MEDLINE=91229699; PubMed=2029337;  
 Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;  
 "Identification of a gene family regulated by transforming growth  
 factor-beta.";  
 DNA Cell Biol. 10:293-300(1991).  
 -1- TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND BRAIN  
 (LOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).  
 -1- INDUCTION: BY GROWTH FACTORS.  
 -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING  
 PROTEIN FAMILY. CEF-10/CYR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.  
 -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.  
 -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).  
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 or send an email to license@isb-sib.ch).  
 -----  
 EMBL; M70641; AAA37627.1; -;  
 EMBL; M70642; AAA37628.1; -;  
 EMBL; M80263; AAA73135.1; -;  
 PIR; A53228; A53228.  
 MGD; MGI:95537; Fisp12.  
 InterPro; IPR000359; -;  
 InterPro; IPR000867; -;  
 InterPro; IPR000884; -;  
 InterPro; IPR001007; -;  
 Pfam; PF00007; Cys\_knot; 1.  
 Pfam; PF00219; IGFBP; 1.  
 Pfam; PF00090; tsp\_1; 1.  
 Pfam; PF00093; vwc; 1.  
 PROSITE; PS00222; IGF\_BINDING; 1.  
 PROSITE; PS01185; CTCK\_1; 1.  
 PROSITE; PS01225; CTCK\_2; 1.  
 PROSITE; PS01208; VWFC; 1.  
 Growth factor binding; Signal.  
 SIGNAL 1 25  
 CHAIN 26 348 CONNECTIVE TISSUE GROWTH FACTOR.  
 DOMAIN 100 166 VWFC.  
 DISULFID 255 329 CTCK.  
 DISULFID 272 306 BY SIMILARITY.  
 DISULFID 283 322 BY SIMILARITY.  
 DISULFID 286 324 BY SIMILARITY.  
 DISULFID 291 328 BY SIMILARITY.  
 CONFLICT 161 161 K -> E (IN REF. 2).  
 SEQUENCE 348 AA; 37793 MW; 735B65B6A711686F CRC64;  
 Query Match 97.78; Score 926; DB 1; Length 348;  
 Best Local Similarity 95.94; Pred. No. 9.7e-76;  
 Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
 1 AAYRLEDTFGDPPTMRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60  
 179 AAYRLEDTFGDPPTMRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 238  
 61 RPEADLEENIKKCKIRTPKISKPKIFELSGCTSMKTYRAKCGVCTDGRCCCTPHRTT 120  
 239 RPEADLEENIKKCKIRTPKIAKPKFELSGCTSVKTYRAKCGVCTDGRCCCTPHRTT 298

QY 121 TLPVEFKCPDGEVAKKNNMFIKTCACHYNCPCDNDIFESLYYRKMYGDM 170  
 DQ 299 TLPVEFKCPDGEVAKKNNMFIKTCACHYNCPCDNDIFESLYYRKMYGDM 348  
 RESULT 4  
 CTGF\_BOVIN  
 ID CTGF\_BOVIN STANDARD; PRT; 349 AA.  
 AC O18739;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.  
 GN CTGF.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Aorta;  
 RA Liliensiek B., Lin Z., Fotsis T., Schimanski M., Bierhaus A.,  
 Kanitz M., Kaufmann G., Schweigert L., Ziegler R., Nawroth P.P.;  
 Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY  
 HUMAN VASCULAR ENDOTHELIAL CELLS. THIS IMMEDIATE-EARLY PROTEIN  
 MAY BIND ONE OF THE PDGF CELL SURFACE RECEPTORS.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING  
 PROTEIN FAMILY. CEF-10/CYR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 VWFC DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).  
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 -----  
 EMBL; AF000137; AAB66596.1; -;  
 InterPro; IPR000359; -;  
 InterPro; IPR000867; -;  
 InterPro; IPR000884; -;  
 InterPro; IPR001007; -;  
 Pfam; PF00007; Cys\_knot; 1.  
 Pfam; PF00219; IGFBP; 1.  
 Pfam; PF00090; tsp\_1; 1.  
 Pfam; PF00093; vwc; 1.  
 PROSITE; PS00222; IGF\_BINDING; FALSE\_NEG.  
 PROSITE; PS01185; CTCK\_1; 1.  
 PROSITE; PS01225; CTCK\_2; 1.  
 PROSITE; PS01208; VWFC; FALSE\_NEG.  
 Growth factor binding; Signal.  
 SIGNAL 1 26 POTENTIAL.  
 CHAIN 27 349 CONNECTIVE TISSUE GROWTH FACTOR.  
 DOMAIN 101 167 VWFC.  
 DISULFID 256 330 CTCK.  
 DISULFID 273 307 BY SIMILARITY.  
 DISULFID 283 325 BY SIMILARITY.  
 DISULFID 292 329 BY SIMILARITY.  
 SEQUENCE 349 AA; 38152 MW; D919023AE40D212E CRC64;  
 Query Match 95.6%; Score 906; DB 1; Length 349;  
 Best Local Similarity 96.5%; Pred. No. 5.9e-74;  
 Matches 164; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 1 AAYRLEDTFGDPPTMRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60  
 179 AAYRLEDTFGDPPTMRANCLVQTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 238  
 61 RPEADLEENIKKCKIRTPKISKPKIFELSGCTSMKTYRAKCGVCTDGRCCCTPHRTT 120  
 239 RPEADLEENIKKCKIRTPKIAKPKFELSGCTSVKTYRAKCGVCTDGRCCCTPHRTT 298

Tue Aug 21 08:16:55 2001

1;

Matches 94; Conservative 22; Mismatches 40; Indels 1; Gaps 1;

Db 180 AAYRLEDTEGPDPTMTRANCQVQTTEWSAISKTCMGISTRTVNDNASCRLKQSRCLCMV 239  
 QY 61 RPEADLEENIKGKKCIKTPKISPIKELSGCTSMKTYRAKFCGCTDGRCCPTPHRTT 120  
 Db 240 RPEADLEENIKGKKCIKTPKISPIKELSGCTSMKTYRAKFCGCTDGRCCPTPHRTT 299  
 QY 121 TLPVEFKCPDGEVYKNNMFIKTCACHYNCPGDNDIFESLYYRKMVGMDA 170  
 Db 300 TLPVEFKCPDGEVYKNNMFIKTCACHYNCPGDNDIFESLYYRKMVGMDA 349

RESULT 5  
 NOV\_COTJA STANDARD; PRT; 353 AA.  
 ID NOV\_COTJA  
 AC P42642;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE NOV PROTEIN PRECURSOR.

NOV.  
 Coturnix coturnix japonica (Japanese quail).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Coturnix.  
 OX NCBI\_TaxID=93934;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RA Weiskirchen R., Bister K.; to the EMBL/GenBank/DBJ databases.  
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL  
 CC GROWTH REGULATION (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING  
 CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.  
 CC -!- SIMILARITY: CONTAINS 1 WFEC DOMAIN.  
 CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).

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CC EMBL; U13063; AAA21128.1; -  
 CC InterPro: IPR000359; -  
 CC InterPro: IPR000867; -  
 CC InterPro: IPR000884; -  
 CC InterPro: IPR001007; -  
 CC Pfam; PF00007; Cys\_knot; 1.  
 CC Pfam; PF00219; IGFBP; 1.  
 CC Pfam; PF00090; tsp\_1; 1.  
 CC Pfam; PF00093; vwc; 1.  
 CC PROSITE; PS00222; IGF\_BINDING; 1.  
 CC PROSITE; PS01185; CTCK\_1; 1.  
 CC PROSITE; PS01225; CTCK\_2; 1.  
 CC PROSITE; PS01208; WFEC; 1.  
 CC Proto-oncogene; Growth factor binding; Signal.  
 KW SIGNAL; 1  
 FT CHAIN 27 353  
 FT DOMAIN 106 172  
 FT DOMAIN 260 334  
 FT DISULFID 260 297  
 FT DISULFID 277 311  
 FT DISULFID 288 327  
 FT DISULFID 291 329  
 FT DISULFID 296 333  
 FT CARBOHYD 276 276  
 FT SEQUENCE 353 AA; 38667 MW; 717D9F8533882E89 CRC64;

Query Match 57.1%; Score 541.5; DB 1; Length 353;  
 Best Local Similarity 59.9%; Pred. NO. 1.8e-41;

RESULT 6

NOV\_CHICK STANDARD; PRT; 351 AA.

ID NOV\_CHICK

AC P28686;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE NOV PROTEIN PRECURSOR.

GN NOV.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus

OX NCBI\_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BROWN LEHORN;

RX MEDLINE=92107157; PubMed=1309586;

RA Joliet V., Martinie C., Dambrie G., Plassiat G., Brisac M.,

RA Crochet J., Perbal B.;

RT "proliferation rearrangements and overexpression of a new cellular gene

(nov) in myeloblastosis-associated virus type 1-induced

nephroblastomas";

RT Mol. Cell. Biol. 12:10-21(1992).

CC -!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL

CC GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WITH

CC TUMORIGENESIS AND EXPRESSION OF A N-TERMINAL-TRUNCATED VERSION

CC OF NOV GENE IN CHICKEN EMBRYONIC FIBROBLASTS (CEF) IS SUFFICIENT

CC TO INDUCE THE TRANSFORMATION OF CEF IN VITRO.

CC -!- TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN

CC MUSCLE AND INTESTINE, IN THE EMBRYO. LUNG AND LESS SO IN BRAIN AND

CC -!- DEVELOPMENTAL STAGE: MAWI-INDUCED NEPHROBLASTOMAS EXPRESS A HIGH

CC LEVEL OF NOV GENE WHOSE TRANSCRIPTION IS NORMALLY ARRESTED IN

CC ADULT KIDNEY.

CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING

CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.

CC -!- SIMILARITY: CONTAINS 1 WFEC DOMAIN.

CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).

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CC EMBL; X59284; CAA41975.1; -  
 CC PIR; S20078; S20078.  
 CC InterPro: IPR000359; -  
 CC InterPro: IPR000867; -  
 CC InterPro: IPR000884; -  
 CC InterPro: IPR001007; -  
 CC Pfam; PF00007; Cys\_knot; 1.  
 CC Pfam; PF00219; IGFBP; 1.  
 CC Pfam; PF00090; tsp\_1; 1.  
 CC Pfam; PF00093; vwc; 1.



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DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS01208; VWFC; 1.
KW Proto-oncogene; Growth factor binding; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 351 NOV PROTEIN.
FT DOMAIN 104 170 VWFC.
FT DOMAIN 258 332 CTCK.
FT DISULFID 258 295 BY SIMILARITY.
FT DISULFID 275 309 BY SIMILARITY.
FT DISULFID 286 325 BY SIMILARITY.
FT DISULFID 289 327 BY SIMILARITY.
FT DISULFID 294 331 BY SIMILARITY.
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 351 AA; 38268 MW; 1ECB3FA3058C6797 CRC64;

Query Match 57.0%; Score 540.5; DB 1; Length 351;
Best Local Similarity 59.9%; Pred. No. 2.3e-41;
Matches 94; Conservative 22; Mismatches 40; Indels 1; Gaps 1;

Qy 1 AAYRLETFGDPDMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRLCMV 60
Db 183 AAYRQETATLGIDVSDSSANCIQETQTSACSKCGMGFSTRVTRNRQOCVMVKOTRLCMW 242
Qy 61 RPEADLEENIKKKKCIPTKISKPIKFSLGCTSMKTYRAKFCGVCCTDCRCCTPHRTT 120
Db 243 RPEENE-EPSPDKGKKCIQTKSKMAYRFEYKNTSVQTYKPRYCGLCNDRGCRCTPHNTK 301
Qy 121 TLPVEFKCPDGEVKNMFKTKCACHYNCPGDNDF 157
Db 302 TIQVEFRCPQCGKFLKPKMLINTCVCHGNCPSQNNAF 338

RESULT 7
NOV_XENLA STANDARD; PRT; 343 AA.
AC P51609;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE NOV PROTEIN HOMOLOG PRECURSOR (XNOV).
GN NOV.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257227; PubMed=8666280;
RA Ying Z., King M.L.;
RT "Isolation and characterization of xnov, a Xenopus laevis ortholog of
RL the chicken nov gene.";
RL Gene 171:243-248(1996).
CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
CC GROWTH REGULATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U37063; AAB17096.1;
DR InterPro; IPR000359; .
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DR InterPro; IPR000867; .
DR InterPro; IPR000884; .
DR InterPro; IPR001007; .
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00219; IGFBP; 1.
DR Pfam; PF00090; tsp_1; 1.
DR Pfam; PF00093; vwc; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS01208; VWFC; 1.
DR PROSITE; PS01185; CTCK_1; FALSE_NEG.
DR PROSITE; PS01225; CTCK_2; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 343 NOV PROTEIN HOMOLOG.
FT DOMAIN 93 159 VWFC.
FT DOMAIN 249 323 CTCK.
FT DISULFID 249 286 BY SIMILARITY.
FT DISULFID 266 300 BY SIMILARITY.
FT DISULFID 277 316 BY SIMILARITY.
FT DISULFID 280 318 BY SIMILARITY.
FT DISULFID 285 322 BY SIMILARITY.
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 343 AA; 38070 MW; 677D7078EB21365F CRC64;

Query Match 54.7%; Score 518.5; DB 1; Length 343;
Best Local Similarity 57.2%; Pred. No. 2e-39;
Matches 91; Conservative 22; Mismatches 45; Indels 1; Gaps 1;

Qy 1 AAYRLETFGDPDMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLEKQSRLCMV 60
Db 172 AAYRPEATLGIDASDTSPACIAQTQTSACSKTCGMGVSSRTVTRNRARCEMQKIRLCMV 231
Qy 61 RPEADLEENI-KGKKCIPTKISKPIKFSLGCTSMKTYRAKFCGVCCTDCRCCTPHRT 119
Db 232 RSCDEEPGWHEKKGKCVRRVTKTKPIHFHYKNTSVQTYKPRYCGLCNDRGCRCTPHST 291
Qy 120 TLPVEFKCPDGEVKNMFKTKCACHYNCPGDNDFE 158
Db 292 KTMHVEFVCPQKRVKPKVMVISTCVCHYNCQDSSLLQ 330

RESULT 8
NOV_HUMAN STANDARD; PRT; 357 AA.
AC P48745;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NOV PROTEIN HOMOLOG PRECURSOR (NOVH).
GN NOV.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=94336229; PubMed=7520150;
RA Martinerie C., Huff V., Joubert I., Badzioch M., Saunders G.,
RA Strong L., Perbal B.;
RT "Structural analysis of the human nov proto-oncogene and expression
RT in Wilms tumor.";
RL Oncogene 9:2729-2732(1994).
CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
CC GROWTH REGULATION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: INCREASED EXPRESSION IN WILMS TUMOR OF THE
CC STROMAL TYPE.
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
CC
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EMBL; X78351; CAA55146.1; JOINED.  
EMBL; X78352; CAA55146.1; JOINED.  
EMBL; X78353; CAA55146.1; JOINED.  
EMBL; X78354; CAA55146.1; JOINED.  
EMBL; X96584; CAA65403.1; -  
MIM; 164958; -  
InterPro; IPR000359; -  
InterPro; IPR000867; -  
InterPro; IPR000884; -  
InterPro; IPR001007; -  
Pfam; PF00007; Cys\_knot; 1.  
Pfam; PF00219; IGF-BP; 1.  
Pfam; PF00090; tsp\_1; 1.  
Pfam; PF00093; vwc; 1.  
PROSITE; PS00222; IGF-BINDING; 1.  
PROSITE; PS01185; CTCK\_1; 1.  
PROSITE; PS01225; CTCK\_2; 1.  
PROSITE; PS01208; VWFC; 1.  
Proto-Oncogene; Growth factor binding; Signal.  
POTENTIAL.  
CHAIN 1 27  
NOV PROTEIN HOMOLOG.  
FT CHAIN 28 357  
FT DOMAIN 108 174  
FT DOMAIN 264 338  
FT DISULFID 264 301  
FT DISULFID 281 315  
FT DISULFID 292 331  
FT DISULFID 295 333  
FT DISULFID 300 337  
FT CARBOHYD 97 97  
FT CARBOHYD 280 280  
SEQUENCE 357 AA; 39162 MW; 035D5BF4576BD85B CRC64;

Query Match 54.3%; Score 515; DB 1; Length 357;  
Best Local Similarity 54.4%; Pred. No. 4.3e-39;  
Matches 93; Conservative 25; Mismatches 51; Indels 2; Gaps 2;  
QY 1 AAYLETFGPDPTMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 60  
DB 187 AAYRPEATLGVEVSDSVNCTEQTTEWTSACSKTCGMGISTRTVNRNRCQEMLKQTRLCMV 246  
QY 61 RPEADLEE-NIKGKKCIPTKISPKIPKELSGCTSMKTYRAKFCGVCCTDGCCTPHRT 119  
DB 247 RPEQEPDPTDKGKKCLRTKSKLKHLOFNKCTSLHTYKPRFCGVCSDGRCCTPHNT 306  
QY 120 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPGNDIF-ESLYYRKMVYGD 169  
DB 307 KTIQAEFCPSQIVKPKVMVIGTCTHTNCPKNEAPLQELKTRGKM 357

RESULT 9  
ID NOV\_MOUSE STANDARD; PRT; 354 AA.  
AC Q64299;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE NOV PROTEIN HOMOLOG PRECURSOR (NOVH).  
OS Mus musculus (Mouse).  
GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-129/SV, AND ICR: TISSUE=Brain;  
RX MEDLINE-97131523; PubMed=8975721;  
RA Snaith M.R., Natarajan D., Taylor L.B., Choi C.P., Martinerie C.,  
RA Perbal B., Schofield P.N., Boulter C.A.;  
RT "Genomic structure and chromosomal mapping of the mouse nov gene";  
RL Genomics 38:425-428(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6;  
RX MEDLINE-96204003; PubMed-8622864;  
RA Martinerie C., Chausse G., Rauscher F.J. III, Perbal B.;  
RA "Regulation of nov by wt1: a potential role for nov in  
RT nephrogenesis";  
RL Oncogene 12:1479-1492(1996).  
CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL  
CC GROWTH REGULATION (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING  
CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).  
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CC -----  
EMBL; X97863; CAA66457.1; -  
EMBL; X99257; CAA70454.1; -  
EMBL; X96585; CAA65404.1; -  
MGI; MGI:109185; Nov.  
InterPro; IPR000359; -  
InterPro; IPR000867; -  
InterPro; IPR000884; -  
InterPro; IPR001007; -  
Pfam; PF00007; Cys\_knot; 1.  
Pfam; PF00219; IGF-BP; 1.  
Pfam; PF00090; tsp\_1; 1.  
Pfam; PF00093; vwc; 1.  
PROSITE; PS00222; IGF-BINDING; 1.  
PROSITE; PS01185; CTCK\_1; 1.  
PROSITE; PS01225; CTCK\_2; 1.  
PROSITE; PS01208; VWFC; 1.  
Proto-Oncogene; Growth factor binding; Signal.  
POTENTIAL.  
CHAIN 1 21  
NOV PROTEIN HOMOLOG.  
FT CHAIN 22 354  
FT DOMAIN 102 168  
FT DOMAIN 261 335  
FT DISULFID 261 298  
FT DISULFID 278 312  
FT DISULFID 289 328  
FT DISULFID 292 330  
FT DISULFID 297 334  
FT CARBOHYD 91 91  
FT CARBOHYD 277 277  
SEQUENCE 354 AA; 38928 MW; 08E8C8FC67829DE CRC64;

Query Match 54.1%; Score 512.5; DB 1; Length 354;  
Best Local Similarity 58.0%; Pred. No. 7.1e-39;  
Matches 91; Conservative 23; Mismatches 42; Indels 1; Gaps 1;  
QY 2 AYRLETFGPDPTMIRANCLVOTTEWSACSKTCGMGISTRTVNDNASCRLKQSLCMV 61  
DB 185 AYRPEATVGVEVSDSVNCTEQTTEWTSACSKTCGMGISTRTVNRNRCQEMLKQTRLCIVR 244  
QY 62 RPEADLEE-NIKGKKCIPTKISPKIPKELSGCTSMKTYRAKFCGVCCTDGCCTPHRT 120  
DB 245 RPEQEPDPTDKGKKCLRTKSKLKHLOFNKCTSLHTYKPRFCGVCSDGRCCTPHNTK 304  
QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPGNDIF 157

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AC 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE 15-DEC-1998 (Rel. 37, Last annotation update)  
 DT NEUTRIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (GDNF  
 DE NEUTRIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (GDNF  
 DE RECEPTOR BETA) (GDNR-BETA) .  
 DE RECEPTOR BETA) (GDNR-BETA) .  
 GF GF2 OR GDNFR.  
 GN GF2 OR GDNFR.  
 GN GF2 OR GDNFR.  
 OS Gallus gallus (Chicken) .  
 OS Gallus gallus (Chicken) .  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OC Gallus.  
 OC Gallus.

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OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97336104; PubMed=9192899;
RA Rosenthal A., Adu J., Pion L.G.P., Horton A., Thompson J.,
RA Bujo-Bello A., Chinchetru M., Buchman V.L., Davies A.M.;
RT "Neuritin responsiveness requires a GPI-linked receptor and the Ret
RT receptor tyrosine kinase."
RL Nature 387:721-724(1997).
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
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CC -----
DR EMBL; U90542; AAB61571.1; -
DR Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 445 NEURTURIN RECEPTOR ALPHA.
FT PROPEP 446 465 HYDROPHOBIC, REMOVED DURING MATURATION
FT (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 445 445 GPI-ANCHOR (POTENTIAL)
SQ SEQUENCE 465 AA; 51908 MW; 22CD9024ED971F06 CRC64;

Query Match 10.7%; Score 101.5; DB 1; Length 465;
Best Local Similarity 25.8%; Pred. No. 0.039;
Matches 47; Conservative 15; Mismatches 61; Indels 59; Gaps 12;

QY 4 RLEDTF-----GDPD-TMIRAN-CLVQTTWSACSKTCGMGISTRVNDNASCRLEQ 54
DB 134 RLSDIFRLASIFSGMDPATNSKSHL-----DAAKACNL-----NDNC-----KR 174
QY 55 SRLCMVRPEADLEENKKGKCKIRTPKISKPFELSGCTSMKYRAKFCGVCTDGRCC 114
DB 175 LRSYISTC-----SKEISATEHCSSR-KCHKALRQFFDNVPSEYTYRLFLCS-CKDQACA 228
QY 115 TPHTTLPVFEKCPDGEVAKKNM-----FIKTCACHY-----NCPG 152
DB 229 EPRQTIQVFP---CSYEDKEKPNCLDLRNVCRADHLCSRLADFHANCQASFSQITSCPG 285
QY 153 DN 154
DB 286 DN 287

RESULT 14
FSPO_RAT STANDARD; PRT; 807 AA.
AC P35446;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE F-SPONDIN PRECURSOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Embryonic floor plate;
RX MEDLINE=92208952; PubMed=1555244;
RA Kiar A., Baldassare M., Jessell T.M.;
RT "F-spondin: a gene expressed at high levels in the floor plate
RT encodes a secreted protein that promotes neural cell adhesion and
RT neurite extension."
RL Cell 69:95-110(1992).
CC -1- FUNCTION: PROMOTES THE ATTACHMENT OF SPINAL CORD AND SENSORY
CC NEURON CELLS AND THE OUTGROWTH OF NEURITES IN VITRO. MAY
CC CONTRIBUTE TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE SPINAL
CC CORD AND THE PNS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE FLOOR PLATE.
CC -1- SIMILARITY: CONTAINS 6 TYPE-1 TSP DOMAINS.
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CC -----
DR EMBL; M88469; AAA41174.1; -
DR PIR; A38152; A38152.
DR InterPro; IPR000884; -
DR InterPro; IPR002861; -
DR Pfam; PF02014; Reeler; 1.
DR Pfam; PF00090; tsp_1; 6.
DR PROSITE; PS00092; TSP1; 5.
KW Glycoprotein; Signal; Repeat; Cell adhesion.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 807 F-SPONDIN.
FT DOMAIN 443 494 TSP TYPE-1 1.
FT DOMAIN 502 554 TSP TYPE-1 2.
FT DOMAIN 559 610 TSP TYPE-1 3.
FT DOMAIN 615 665 TSP TYPE-1 4.
FT DOMAIN 669 720 TSP TYPE-1 5.
FT DOMAIN 755 807 TSP TYPE-1 6.
FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 681 681 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 807 AA; 90773 MW; 309525F9EAFE89A CRC64;

Query Match 10.7%; Score 101.5; DB 1; Length 807;
Best Local Similarity 24.7%; Pred. No. 0.065;
Matches 42; Conservative 19; Mismatches 46; Indels 63; Gaps 10;

QY 18 ANCLV-QTTWSACSKTCGMGISTR-----VTNDNASCRLE-KOSRLCMVRPCE----- 64
DB 557 SSCLVTWGEWDDCSATCGMGKRRHRVMKSPADGSMCKAETSQAECMMPECHTIPCL 616
QY 65 -----ADLEENIKKCKIRTPKISKPFELSG 93
DB 617 LSPWSEWSDCSVTGKGMRTQRMLKSLAELGDCNEDLEQAEKCM-LPEC--PIDCELS 673
QY 94 CTSMTKYRAKFCGVCTDGRCCTPH--RTTLPVE-----FKCPDGEVAKK 136
DB 674 WSQWSECN-KSCG-----KGHMIRTRTIQMEPQFGGAPCPETVQRKK 714

RESULT 15
FSPO_XENLA STANDARD; PRT; 803 AA.
AC P35447;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE F-SPONDIN PRECURSOR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.

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Tue Aug 21 08:16:55 2001

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OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=93376785; PubMed=8367492;
RA Ruiz I Altaba A., Cox C., Jessell T.M., Klar A.;
RT "Ectopic neural expression of a floor plate marker in frog embryos
RL injected with the midline transcription factor pntallavis.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:8268-8272(1993).
CC -1- FUNCTION: PROMOTES THE ATTACHMENT OF SPINAL CORD AND SENSORY
CC NEURON CELLS AND THE OUTGROWTH OF NEURITES IN VITRO. MAY
CC CONTRIBUTE TO THE GROWTH AND GUIDANCE OF AXONS IN BOTH THE SPINAL
CC CORD AND THE PNS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE FLOOR PLATE.
CC -1- SIMILARITY: CONTAINS 6 TYPE-1 TSP DOMAINS.
CC -----
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CC -----
DR EMBL; L09123; AAA19105.1; -
DR PIR; A47723; A47723.
DR InterPro; IPR000884; -
DR InterPro; IPR002861; -
DR Pfam; PF02014; Reeler; 1.
DR Pfam; PF00090; tsp-1; 6.
DR PROSITE; PS50092; TSP1; 6.
KW Glycoprotein; Signal; Repeat; Cell adhesion.
FT SIGNAL 1 23
FT CHAIN 24 803
FT DOMAIN 437 488 TSP TYPE-1 1.
FT DOMAIN 496 548 TSP TYPE-1 2.
FT DOMAIN 553 604 TSP TYPE-1 3.
FT DOMAIN 609 661 TSP TYPE-1 4.
FT DOMAIN 665 716 TSP TYPE-1 5.
FT DOMAIN 751 803 TSP TYPE-1 6.
FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 677 677 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 803 AA; 90702 MW; D3A54E329548AED9 CRC64;

Query Match 10.4%; Score 99; DB 1; Length 803;
Best Local Similarity 26.8%; Pred. No. 0.11; Indels 22; Gaps 6;
Matches 38; Conservative 18; Mismatches 64;

QY 21 LVQTTWSACSKTCGMG--ISFRTN-----DNASCRLEKOSRLQWVRPCE---ADLEEN 70
DB 667 LTEWSYSECNKSCGKGMHIRTMTPEPQGGAVCFVQRKKCLRKCKQKSSGNERH 726
QY 71 IKKGKKIRTPKIPKIFELSGCTSMKTYRA-----KFCGVCVDGRCCPTPHRTILPVE 125
DB 727 LKDAKRRSEKIKEDSDGEQYPCVKMKPWTAWTECTKFCGGIQERFMTVKRKFSQF 786
QY 126 FKCPDGEVMKKNMFIKTCACH 147
DB 787 TSCKD----KKE---IRACNVH 801
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Search completed: August 20, 2001, 22:57:00  
Job time: 545 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 20, 2001, 22:46:30 ; Search time 93.5 seconds  
(without alignments)  
240.555 Million cell updates/sec

Title: US-09-461-646-2\_COPY\_180\_349

Perfect score: 948

Sequence: 1 AAYRLEDTFGPDPTMIRANC.....PGDNDFESLYRKMYGDMA 170

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL\_16.\*

2: sp\_archaea.\*

3: sp\_bacteria.\*

4: sp\_fungi.\*

5: sp\_human.\*

6: sp\_invertebrate.\*

7: sp\_mammal.\*

8: sp\_mhc.\*

9: sp\_organelle.\*

10: sp\_phase.\*

11: sp\_plant.\*

12: sp\_rodent.\*

13: sp\_unclassified.\*

14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	935	98.6	349	6	Q97765 sus scrofa
2	930	98.1	349	6	Q9GL71 Q9GL71 bos taurus
3	926	97.7	347	11	Q9WVS1 Q9WVS1 rattus norv
4	926	97.7	347	11	Q9RIE9 Q9RIE9 rattus norv
5	891	94.0	343	13	Q42607 Q42607 xenopus lae
6	885	93.4	347	13	Q9PT80 Q9PT80 notophthalm
7	566	59.7	113	11	Q9Z164 Q9Z164 rattus norv
8	499	52.6	351	11	Q9QZQ5 Q9QZQ5 rattus norv
9	489.5	51.6	379	11	Q9ES72 Q9ES72 rattus norv
10	487.5	51.4	379	11	Q9WTM9 Q9WTM9 rattus norv
11	485.5	51.2	381	4	Q43775 Q43775 homo sapien
12	423	44.6	367	11	O54775 O54775 mus musculu
13	404	42.6	331	4	O95958 O95958 homo sapien
14	404	42.6	354	4	O95389 O95389 homo sapien
15	402.5	42.5	334	4	Q9UID7 Q9UID7 homo sapien
16	400.5	42.2	280	4	Q9HCS3 Q9HCS3 homo sapien
17	400.5	42.2	367	4	O95388 O95388 homo sapien
18	352	37.1	70	13	Q9DF21 Q9DF21 scylliorhinu
19	236	24.9	128	11	Q9R2C0 Q9R2C0 rattus norv

20	191	20.1	179	5	Q9VVK0 Q9VVK0 drosophila
21	190	20.0	58	6	O97574 O97574 bos taurus
22	148	15.6	250	4	O76076 O76076 homo sapien
23	146	15.4	251	11	Q9ZOG4 Q9ZOG4 mus musculu
24	144	15.2	250	11	Q9JHC6 Q9JHC6 rattus norv
25	123	13.0	100	4	O9UDL6 O9UDL6 homo sapien
26	116	12.2	2165	5	O19791 O19791 caenorhabdi
27	108.5	11.4	1054	5	O9W493 O9W493 drosophila
28	107	11.3	176	13	O9PSS6 O9PSS6 gallus gall
29	107	11.3	1444	5	Q17591 Q17591 caenorhabdi
30	106.5	11.2	425	6	O02661 O02661 bos taurus
31	105.5	11.1	687	5	Q23729 Q23729 cryptospori
32	102.5	10.8	2098	5	Q25757 Q25757 plasmodium
33	102.5	10.8	2114	5	O97267 O97267 plasmodium
34	101.5	10.7	1235	4	O95428 O95428 homo sapien
35	101	10.7	807	4	O9HC86 O9HC86 homo sapien
36	100.5	10.6	808	13	O42113 O42113 brachydania
37	100.5	10.6	1081	5	O9U631 O9U631 drosophila
38	100.5	10.6	1083	5	O9VTT0 O9VTT0 drosophila
39	99	10.4	712	5	O43981 O43981 eimeria ten
40	98	10.3	769	11	O9QXT7 O9QXT7 mus musculu
41	97	10.2	445	4	O43384 O43384 homo sapien
42	97	10.2	1290	4	Q9UP26 Q9UP26 homo sapien
43	96.5	10.2	432	4	O9NPM2 O9NPM2 homo sapien
44	96.5	10.2	654	5	Q19284 Q19284 caenorhabdi
45	96.5	10.2	898	4	Q9UFZ4 Q9UFZ4 homo sapien

## ALIGNMENTS

RESULT 1

ID O97765 PRELIMINARY: PRT; 349 AA.  
AC O97765;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE CONNECTIVE TISSUE GROWTH FACTOR.  
GN CTGF.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=UTERUS;  
RA Harding P.A., Brigstock D.R.;  
RT "Cloning and sequencing of a porcine connective tissue growth factor  
(CTGF) cDNA."  
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U70060; AD00174.1; -;  
DR InterPro; IPR000359; -;  
DR InterPro; IPR000867; -;  
DR InterPro; IPR001007; -;  
DR Pfam; PF00007; Cys\_knot; 1.  
DR Pfam; PF00090; tsp\_1; 1.  
DR Pfam; PF00093; vwc; 1.  
DR Pfam; PF00219; IGFBP; 1.  
DR PROSITE; PS01185; CTCK\_1; 1.  
DR PROSITE; PS01225; CTCK\_2; 1.  
DR PROSITE; PS00222; IGF\_BINDING; 1.  
DR PROSITE; PS01208; VWFC; 1.  
DR SMART; SM00041; CT; 1.  
SQ SEQUENCE 349 AA; 37946 MW; 35AB4275AC1D4B3A CRC64;

Query Match 98.6%; Score 935; DB 6; Length 349;  
Best Local Similarity 97.6%; Pred. No. 8.2e-93;  
Matches 166; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYRLEDTFGPDPTMIRANCLVQTTESACSKTCGMSGISTRTVNDNASCRLEKQSRCLMW 60

Tue Aug 21 08:16:55 2001

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Db 180 AAYRLEDTFGPDTMIRANCLVQTTWSSACSKTCGMGISTRTVNDNASCRLKQSRCLMV 239
QY 61 RPEADLEENIKKGGKCIKTPKISKPIKPFELSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 120
Db 240 RPEADLEENIKKGGKCIKTPKISKPIKPFELSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 299
QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPCGNDIFESLYYRKMVGMDMA 170
Db 300 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPCGNDIFESLYYRKMVGMDMA 349
RESULT 2
ID Q9GL71 PRELIMINARY; PRT; 349 AA.
AC Q9GL71;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.
GN CTGF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Liver;
RA Mathias M., Schwitters C., Hove M., Rupp S., Brundu N.E.;
RT "Bovine connective tissue growth factor, organization of the
RT chromosomal gene and demonstration of promoter activity.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309555; RAG30290.1; 37924 MW; 5FFC8EE83EFB4F99 CRC64;
SQ SEQUENCE 349 AA; 37924 MW; 37924 MW; 5FFC8EE83EFB4F99 CRC64;

Query Match 98.1%; Score 930; DB 6; Length 349;
Best Local Similarity 98.2%; Pred. No. 2.8e-92;
Matches 167; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDTMIRANCLVQTTWSSACSKTCGMGISTRTVNDNASCRLKQSRCLMV 60
Db 180 AAYRLEDTFGPDTMIRANCLVQTTWSSACSKTCGMGISTRTVNDNASCRLKQSRCLMV 239
QY 61 RPEADLEENIKKGGKCIKTPKISKPIKPFELSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 120
Db 240 RPEADLEENIKKGGKCIKTPKISKPIKPFELSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 299
QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPCGNDIFESLYYRKMVGMDMA 170
Db 300 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPCGNDIFESLYYRKMVGMDMA 349
RESULT 3
ID Q9WVS1 PRELIMINARY; PRT; 347 AA.
AC Q9WVS1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CONNECTIVE TISSUE GROWTH FACTOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Tezuka K., Tamatani T.;
RT "Rattus norvegicus connective tissue growth factor.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB023068; BAA82125.1;
DR InterPro; IPR000072;

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DR InterPro; IPR000359;
DR InterPro; IPR000867;
DR InterPro; IPR000884;
DR InterPro; IPR001007;
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00090; tsp_1; 1.
DR Pfam; PF00093; vwc; 1.
DR Pfam; PF00219; IGFBP; 1.
DR Pfam; PF001629; 1.
DR PRODOM; PD001629; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS01208; VWFC; 1.
DR SMART; SM00041; CT; 1.
SQ SEQUENCE 347 AA; 37837 MW; 6A69511DE72FBF1C CRC64;

Query Match 97.7%; Score 926; DB 11; Length 347;
Best Local Similarity 95.9%; Pred. No. 7.6e-92;
Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDTMIRANCLVQTTWSSACSKTCGMGISTRTVNDNASCRLKQSRCLMV 60
Db 178 AAYRLEDTFGPDTMIRANCLVQTTWSSACSKTCGMGISTRTVNDNASCRLKQSRCLMV 237
QY 61 RPEADLEENIKKGGKCIKTPKISKPIKPFELSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 120
Db 238 RPEADLEENIKKGGKCIKTPKISKPIKPFELSGCTSMKTYRAKFCGCTDGRCCCTPHRTT 297
QY 121 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPCGNDIFESLYYRKMVGMDMA 170
Db 298 TLPVEFKCPDGEVNMKNMFIKTCACHYNCPCGNDIFESLYYRKMVGMDMA 347
RESULT 4
ID Q9RIE9 PRELIMINARY; PRT; 347 AA.
AC Q9RIE9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CONNECTIVE TISSUE GROWTH FACTOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Xu J., Smock S.L., Rosenzweig A.B., Odgren P.R., Safadi F.F.,
RC Marks S.C., Jr., Owen T.A., Popoff S.N.;
RT "Cloning of the cDNA for Rat Connective Tissue Growth Factor (CTGF):
RT Implications for Skeletal Development.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF120275; AAD39132.1;
DR InterPro; IPR000359;
DR InterPro; IPR000867;
DR InterPro; IPR000884;
DR InterPro; IPR001007;
DR Pfam; PF00007; Cys_knot; 1.
DR Pfam; PF00090; tsp_1; 1.
DR Pfam; PF00093; vwc; 1.
DR Pfam; PF00219; IGFBP; 1.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00222; IGF_BINDING; 1.
DR PROSITE; PS01208; VWFC; 1.
DR SMART; SM00041; CT; 1.
SQ SEQUENCE 347 AA; 37756 MW; CFBELAI9766B7B16 CRC64;

Query Match 97.7%; Score 926; DB 11; Length 347;
Best Local Similarity 95.9%; Pred. No. 7.6e-92;
Matches 163; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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QY 1 AAYRLEDTFGPDMIRANCLVQTTWASCKTTCGMISTRVTNDNASCRLKQSLCMV 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 178 AAYRLEDTFGPDMIRANCLVQTTWASCKTTCGMISTRVTNDNASCRLKQSLCMV 237
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RPEADLEENIKGKKIRTPKISKPIKFSGLSGTSMKTYRAKFCGCTDGRCCTPHRTT 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 238 RPEADLEENIKGKKIRTPKISKPIKFSGLSGTSMKTYRAKFCGCTDGRCCTPHRTT 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 170
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 298 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
ID O42607 PRELIMINARY; PRT; 343 AA.
AC O42607;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE CONNECTIVE TISSUE GROWTH FACTOR XCTGF.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying Z., King M.L.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U43524; AAB67639.1; -.
DR EMBL: U43523; AAB67638.1; -.
DR InterPro: IPR000359; -.
DR InterPro: IPR000867; -.
DR InterPro: IPR000884; -.
DR InterPro: IPR001007; -.
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00093; vwc; 1.
DR Pfam: PF00219; IGRBP; 1.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS02022; IGF-BINDING; 1.
DR PROSITE: PS01208; VMFC; UNKNOWN_1.
DR SMART: SM00041; CT; 1.
SQ SEQUENCE 343 AA; 37966 MW; 93F221C5DB565A81 CRC64;

Query Match 94.08; Score 891; DB 13; Length 343;
Best Local Similarity 91.1%; Pred. No. 4.4e-88;
Matches 154; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 2 AYRLEDTFGPDMIRANCLVQTTWASCKTTCGMISTRVTNDNASCRLKQSLCMV 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 175 AFMEETGPDPSLRANCLVQTTWASCKTTCGMISTRVTNDNASCRLKQSLCMV 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 PCEADLEENIKGKKIRTPKISKPIKFSGLSGTSMKTYRAKFCGCTDGRCCTPHRTT 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 235 PCEADLEENIKGKKIRTPKISKPIKFSGLSGTSMKTYRAKFCGCTDGRCCTPHRTT 294
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 122 LPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 170
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 295 LPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 343
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
ID Q9PT80 PRELIMINARY; PRT; 347 AA.
AC Q9PT80;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE CONNECTIVE TISSUE GROWTH FACTOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Murphy M., Godson C., Cannon S., Kato S., Mackenzie H.S., Martin F.,
RA Brady H.R.;
RL "Suppression subtractive hybridization identifies high glucose levels
RT as a stimulus for expression of connective tissue growth factor and
other genes in human mesangial cells.";
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GN CTGF.
OS Notoptthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae;
OC Notoptthalmus
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-FORELIMB BLASTEMA;
RA Gates P.B.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-FORELIMB BLASTEMA;
RX MEDLINE=99033008; PubMed=9813273;
RA Cash D.E., Gates P.B., Imokawa Y., Brookes J.P.;
RT "Identification of newt connective tissue growth factor as a target of
retinoid regulation in limb blastema cells.";
RL Gene 222:119-124 (1998).
DR EMBL: AJ271167; CAB65965.1; -.
DR InterPro: IPR000359; -.
DR InterPro: IPR000867; -.
DR InterPro: IPR000884; -.
DR InterPro: IPR001007; -.
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00093; vwc; 1.
DR Pfam: PF00219; IGRBP; 1.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS02022; IGF-BINDING; 1.
DR PROSITE: PS01208; VMFC; UNKNOWN_1.
DR SMART: SM00041; CT; 1.
SQ SEQUENCE 347 AA; 38098 MW; 3B7E2399F27672C1 CRC64;

Query Match 93.4%; Score 885; DB 13; Length 347;
Best Local Similarity 91.2%; Pred. No. 2e-87;
Matches 155; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 AAYRLEDTFGPDMIRANCLVQTTWASCKTTCGMISTRVTNDNASCRLKQSLCMV 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 178 AVYRQETGPDPSLRANCLVQTTWASCKTTCGMISTRVTNDNASCRLKQSLCMV 237
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 RPEADLEENIKGKKIRTPKISKPIKFSGLSGTSMKTYRAKFCGCTDGRCCTPHRTT 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 238 RPEADLEENIKGKKIRTPKISKPIKFSGLSGTSMKTYRAKFCGCTDGRCCTPHRTT 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 170
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 298 TLPVEFKCPDGEVMMKMMFIKTCACHYNCPCDNDIFESLYRKMVGMA 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
ID Q9Z164 PRELIMINARY; PRT; 113 AA.
AC Q9Z164;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DE CONNECTIVE TISSUE GROWTH FACTOR (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99150373; PubMed=10026205;
RA Murphy M., Godson C., Cannon S., Kato S., Mackenzie H.S., Martin F.,
RA Brady H.R.;
RL "Suppression subtractive hybridization identifies high glucose levels
RT as a stimulus for expression of connective tissue growth factor and
other genes in human mesangial cells.";
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J. Biol. Chem. 274:5830-5834 (1999).  
 EMBL; AF079531; AAD02838.1; -  
 InterPro; IPR000359; -  
 Pfam; PF00007; Cys\_knot; 1.  
 PROSITE; PS01225; CTCK\_2; 1.  
 SMART; SM00041; CT; 1.  
 NON\_TER 1 113  
 NON\_TER 113 113  
 SEQUENCE 113 AA; 12767 MW; 23EA69FCOA60635E CRC64;  
 Query Match 59.7%; Score 566; DB 11; Length 113;  
 Best Local Similarity 93.5%; Pred. No. 1.5e-53;  
 Matches 101; Conservative 4; Mismatches 0; Gaps 0;  
 QY 38 ISTRVNDNASCRLEKQSLCVRCEADLENIKKKKCIPTPKISPIKPFELSGCTSM 97  
 DB 1 ISTRVNDNFTCRLEKQSLCVRCEADLENIKKKKCIPTPKIAKPVKFSCTSV 60  
 QY 98 KTYRAKFCGVCCTGRCCTPHRTTTLPVEFKCPDGEVYKNNMFIKTC 145  
 DB 61 KTYRAKFCGVCCTGRCCTPHRTTTLPVEFKCPHGEIMKNNMFIKTC 108  
 RESULT 8  
 Q9QZQ5 PRELIMINARY; PRT; 351 AA.  
 ID Q9QZQ5  
 AC Q9QZQ5  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-MAY-2001 (T-EMBLrel. 16, Last annotation update)  
 DE NOV PROTEIN.  
 GN NOV.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=20035752; PubMed=10570975;  
 RA Liu C., Liu X.-J., Crowe P.D., Kelnner G.S., Fan J., Barry G., Manu F.,  
 RA Ling N., De Souza E.B., Maki R.A.;  
 RA "Nephroblastoma overexpressed gene (NOV) codes for a growth factor  
 RT that induces protein tyrosine phosphorylation.";  
 RL Gene 338:471-478 (1999).  
 DR EMBL; AF171936; AAD49371.1; -  
 DR InterPro; IPR000359; -  
 DR InterPro; IPR000867; -  
 DR InterPro; IPR000884; -  
 DR InterPro; IPR001007; -  
 DR Pfam; PF00007; Cys\_knot; 1.  
 DR Pfam; PF00090; tsp\_1; 1.  
 DR Pfam; PF00093; vwc; 1.  
 DR Pfam; PF00219; IGFBP; 1.  
 DR PROSITE; PS01185; CTCK\_1; 1.  
 DR PROSITE; PS01225; CTCK\_2; 1.  
 DR PROSITE; PS00222; IGF\_BINDING; 1.  
 DR PROSITE; PS01208; VWFC; UNKNOWN\_1.  
 DR SMART; SM00041; CT; 1.  
 DR SEQUENCE 351 AA; 38509 MW; 02619707DE7C1BFB CRC64;  
 Query Match 52.6%; Score 499; DB 11; Length 351;  
 Best Local Similarity 53.5%; Pred. No. 7.5e-46;  
 Matches 91; Conservative 26; Mismatches 51; Indels 2; Gaps 2;  
 QY 2 AYRLDTFGDPDMIRANCLVOTTEWSACSKTCGMISTRVNDNASCRLEKQSLCVR 61  
 DB 182 AYRPEATVGVELSDSSINCIEQTTEWSACSKSCGMGLSTRVNRNLOCEWVQTRLCV 241  
 QY 62 PCEADL-EEENIKKKKCIPTPKISPIKPFELSGCTSMKTYRAKFCGVCCTGRCCTPHRTT 120

QY	9	FGDPPTMI-----RANCLVQTTTWSACS	KTGCGIGISTRVTNDNASRLEKQSR	LCMVRC	63
		:::			
Db	213	FGMEPRILYNPLOGOKCI	VOTTSMSQCSKTGCGIGISTRVTNDNPN	CECLVKETRICEVRC	272
QY	64	EADLEENIKGKKCI	RTPKISKIKELSGCTSMKTYRAKFGV	CTDGRCCCPHRTTLP	123
		:	:::		
Db	273	GQPVSYSLKGGKCS	TKKSPKRVFTYAGCLSVKKRYPKYG	CGVDCGRCCTPQLTRTVK	332
QY	124	VEFKCPDGEVKKNM	FIKTCACHYNCPCGNDIFESILYR	KMYGDM	169
		:			
Db	333	MRFCDEGETFSK	NVMIQSCKCNYNCPHANEAAFFPY	--RLFNDI	376
RESULT	12				
ID	054775	PRELIMINARY;	PRT;	367	AA.
AC	054775;				
DT	01-JUN-1998	(TReMBLrel. 06, Created)			
DT	01-JUN-1998	(TReMBLrel. 06, Last sequence update)			
DE	01-MAR-2001	(TReMBLrel. 16, Last annotation update)			
DT	ELM1				
GN	ELM1	OR WISPL.			
OS	Mus musculus	(Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID	10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=HEN;				
RX	MEDLINE=98119879; PubMed=9449709;				
RA	Hashimoto Y., Shindo-okada N., Tani M., Nagamachi Y., Takeuchi K.,				
RA	Shiroishi T., Toma H., Yokota J.;				
RT	"Expression of the Eln1 gene, a novel gene of the CCN (connective				
RT	tissue growth factor, Cyr61/Cer10, and neuroblastoma overexpressed				
RT	gene) family, suppresses in vivo tumor growth and metastasis of K-173				
RT	murine melanoma cells.";				
RT	J. Exp. Med. 187:289-296(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=MAMMARY;				
RX	MEDLINE=99061933; PubMed=9843955;				
RA	Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J.,				
RA	Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen R.L.,				
RA	Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan K.J.,				
RA	Gurney A.L., Botstein D., Levine A.J.;				
RT	"WISP genes are members of the connective tissue growth factor family				
RT	that are up-regulated in wnt-1-transformed cells and aberrantly				
RT	expressed in human colon tumors.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).				
DR	EMBL; AB004873; BAA24949.1; -				
DR	EMBL; AF100777; AAC96319.1; -				
DR	MGd; MGI:1197008; Wispl.				
DR	InterPro; IPR000359; -				
DR	InterPro; IPR000867; -				
DR	InterPro; IPR000884; -				
DR	InterPro; IPR001007; -				
DR	Pfam; PF00090; tsp_1; 1.				
DR	Pfam; PF00093; vwc; 1.				
DR	Pfam; PF00219; IGFBP; 1.				
DR	PROSITE; PS01185; CTCK_1; 1.				
DR	PROSITE; PS01225; CTCK_2; 1.				
DR	PROSITE; PS01208; WFC; UNKNOWN_1.				
DR	SMART; SM00041; Ctr; 1.				
SQL	SEQUENCE	367	AA;	40702	MM; 3B7C0569EFAB5E96 CRC64;

Query Match 44.6%; Score 423; DB 11; Length 367;

Best Local Similarity 47.9%; Pred. No. 1.2e-37;

Matches 68; Conservative 31; Mismatches 43; Indels 0; Gaps

QY	19	NCLVQTTTWSACSKT	CGMGIGISTRVTNDNASRLEKQSR	LCMVRCPCADLEENIKGKKCI	78
		:::			

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.Db 215 NCIAVTPSPSCSTCGLGISTRISNVNARCWPEQSRCLNLRPCDVIDIOLHIKAGKKCL 274
QY 79 RTPKISPIKIFELSGTSMKTYRAKFCGVCCTGRCCTPHRTTLPVEFKCPDGEVMKKNM 138
Db 275 AVYQPEATNFTLAGCVSTYRKYKCGVCTDRNCIPYKSKTISVDFQCPEGPGSRQV 334
QY 139 MFIKTCACHYNGCDNDIFESL 160
Db 335 LWINACFCNLSCRPNDFADL 356

RESULT 13
O95958 PRELIMINARY; PRT; 331 AA.
AC O95958;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE DJ142L7.3 (CONNECTIVE TISSUE GROWTH FACTOR (NOV, GIG) LIKE PROTEIN)
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=BONE MARROW, AND FETAL KIDNEY;
RC MEDLINE=99061933; PubMed=9843955;
RX Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J.,
RA Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen R.L.,
RA Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan K.J.,
RA Gurney A.L., Botstein D., Levine A.J.;
RT "Wisp genes are members of the connective tissue growth factor family
RT that are up-regulated in wnt-1-transformed cells and aberrantly
RT expressed in human colon tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).
DR EMBL: AF100781; AAC96323.1;
DR InterPro: IPR000359;
DR InterPro: IPR000867;
DR InterPro: IPR000884;
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00219; IGFBP; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR SMART: SM00041; CT; 1.
DR SMART: SM00041; CT; 1.
SQ SEQUENCE 354 AA; 39292 MW; 67F48D0D5C2F5EE3 CRC64;

(2)
SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA van Golen K.L., Davies S., Wu Z.F., Wang Y.F., Bucana C.D., Root H.,
RA Chandrasekharappa S., Strawderman M., Ehler S.P., Merajver S.D.;
RT "A novel putative IGF-binding, tumor suppressor protein, Libc, and
RT rhoC Gpase, are determinants of the inflammatory breast cancer
RT phenotype";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z99289; CAB16556.1;
DR EMBL: AF143679; AAD31517.1;
DR InterPro: IPR000359;
DR InterPro: IPR000867;
DR InterPro: IPR000884;
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00219; IGFBP; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR SMART: SM00041; CT; 1.
DR SMART: SM00041; CT; 1.
FT NON_TER 331
SQ SEQUENCE 331 AA; 36909 MW; D109C2FDCA1DF549 CRC64;
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Query Match 42.6%; Score 404; DB 4; Length 331;
Best Local Similarity 42.2%; Pred. No. 1.2e-35;
Matches 68; Conservative 37; Mismatches 55; Indels 2; Gaps 1;

QY 2 AYRLDTFGDPTMIRANCLVQTTENSACSKTCGMGISTRTVNDNASCRLKQSLCMVR 61
Db 168 SYKTPAYRNLPILWKKKCLVQATKTPCSTCGMISNRTVNSNCENRKRCLCYIQ 227
QY 62 PCADLEENIK--KGKKCIPTPKISPIKELSGTSMKTYRAKFCGVCCTGRCCTPHRT 119
Db 228 PCDSNLIKTIKIPKGTCTQPTFOLSKRAEKFVFGSCSSTQSYKPTFCGICLDKRCIPNKS 287
QY 120 TTLPVEFKCPDGEVMKKMMFIKTCACHYNGCDNDIFESL 160
Db 288 KMITIQDCPNEGSEFKWMLWITSCVCQRCNCRPGDIFSEL 328

RESULT 14
O95389 PRELIMINARY; PRT; 354 AA.
ID O95389
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O95389;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CONNECTIVE TISSUE GROWTH FACTOR RELATED PROTEIN WISP-3.
GN WISP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW, AND FETAL KIDNEY;
RX MEDLINE=99061933; PubMed=9843955;
RA Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J.,
RA Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen R.L.,
RA Melham M.F., Finley G.G., Quirke P., Goddard A.D., Hillan K.J.,
RA Gurney A.L., Botstein D., Levine A.J.;
RT "Wisp genes are members of the connective tissue growth factor family
RT that are up-regulated in wnt-1-transformed cells and aberrantly
RT expressed in human colon tumors.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).
DR EMBL: AF100781; AAC96323.1;
DR InterPro: IPR000359;
DR InterPro: IPR000867;
DR InterPro: IPR000884;
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00219; IGFBP; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR SMART: SM00041; CT; 1.
DR SMART: SM00041; CT; 1.
SQ SEQUENCE 354 AA; 39292 MW; 67F48D0D5C2F5EE3 CRC64;

Query Match 42.6%; Score 404; DB 4; Length 354;
Best Local Similarity 42.2%; Pred. No. 1.3e-35;
Matches 68; Conservative 37; Mismatches 54; Indels 2; Gaps 1;

QY 2 AYRLDTFGDPTMIRANCLVQTTENSACSKTCGMGISTRTVNDNASCRLKQSLCMVR 61
Db 191 SYKTPAYRNLPILWKKKCLVQATKTPCSTCGMISNRTVNSNCENRKRCLCYIQ 250
QY 62 PCADLEENIK--KGKKCIPTPKISPIKELSGTSMKTYRAKFCGVCCTGRCCTPHRT 119
Db 251 PCDSNLIKTIKIPKGTCTQPTFOLSKRAEKFVFGSCSSTQSYKPTFCGICLDKRCIPNKS 310
QY 120 TTLPVEFKCPDGEVMKKMMFIKTCACHYNGCDNDIFESL 160
Db 311 KMITIQDCPNEGSEFKWMLWITSCVCQRCNCRPGDIFSEL 351

RESULT 15
O95389 PRELIMINARY; PRT; 334 AA.
ID O95389
AC O95389;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CYR61 PROTEIN.
GN CYR61.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 1-107 FROM N.A.
RC TISSUE=KIDNEY;
RA Anding B., Long Y.;
RT "Cloning of a new gene down-regulated in the small-cell tumor
RT embryonal-rhabdomyosarcoma (RMS).";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF003114; AAF21597.1;
DR EMBL: AF003114; AAF21597.1;
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DR InterPro: IPR000359; -
DR InterPro: IPR000867; -
DR InterPro: IPR000884; -
DR InterPro: IPR001007; -
DR Pfam: PF00007; Cys_knot; 1.
DR Pfam: PF00090; tsp_1; 1.
DR Pfam: PF00093; wsc; 1.
DR Pfam: PF00219; IGFBP; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS01208; VWFC; 1.
DR SMART: SM00041; CT; 1.
SQ SEQUENCE 334 AA; 37246 MW; 9188987A7352E948 CRC64;

Query Match 42.5%; Score 402.5; DB 4; Length 334;
Best Local Similarity 45.7%; Pred. No. 1.8e-35;
Matches 79; Conservative 26; Mismatches 47; Indels 21; Gaps 6;

Qy 9 FGPDPTMIRAN-----CLVQTTEWSAGSKTCGGMGISTRTVNDNASCRLEKQSLCMYRP 62
   || : || | | : || || || || || || || || || || || || || || || || ||
Db 166 FGMEP-RIRYNPLQKQKCIIVQTTWSQCSKTCGTGISTRTVNDNPECRLVKETRICEVRP 224
   | : : : || || || | : || : | | | | | | | | | | | | | | | | | |
Qy 63 CEADLEENIKKGKCIPTPKISKPIKELSGCTSMKTYRAKFCGVCCTDGRCTPHRTTTL 122
   | : : : || || || | : || : | | | | | | | | | | | | | | | | | |
Db 225 CGQVYSSLKKGKCKSKPKSPVRFYAGCLSVKRYRPKYCGSCVDGRCTPOLTRT- 283
   | : : : | : | : | : || || | : | : || | : | : || | : | : || |
Qy 123 PVEFKCPDGEVMKK-NMFIK-----TCACHYNCPGDNDIFESLYRYRMYGDM 169
   | : : : | : | : | : || || | : | : || | : | : || | : | : || |
Db 284 -----CEDAVPLRRWGDIFQERHDDPVLKCNYNCPHANEAAFPFY--RLFNDI 329
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Search completed: August 20, 2001, 22:55:51  
Job time: 561 sec

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